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Search for

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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software. It is implemented on hardware provided by HP.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query length: 448 AA (of which 4% low-complexity regions filtered out)
Date run: 2004-03-29 12:03:12 UTC+0100 on sib-gml.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,423,080 sequences; 454,374,568 total letters

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Pseudomonas

	Db AC	Description	Score	E-value
<input type="checkbox"/>	sp Q9HVZ9	MURD_PSEAE UDP-N-acetylmuramoylalanine--D-glutamate li...	839	0.0
<input type="checkbox"/>	sp Q87WY3	MURD_PSESM UDP-N-acetylmuramoylalanine--D-glutamate li...	676	0.0
<input type="checkbox"/>	sp Q88N78	MURD_PSEPK UDP-N-acetylmuramoylalanine--D-glutamate li...	675	0.0
<input type="checkbox"/>	tr Q83F20	UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]...	365	e-100
<input type="checkbox"/>	sp Q8ZRU4	MURD_SALTY UDP-N-acetylmuramoylalanine--D-glutamate li...	354	1e-96
<input type="checkbox"/>	sp Q8Z9H0	MURD_SALTI UDP-N-acetylmuramoylalanine--D-glutamate li...	354	1e-96
<input type="checkbox"/>	sp P14900	MURD_ECOLI UDP-N-acetylmuramoylalanine--D-glutamate li...	353	4e-96
<input type="checkbox"/>	sp Q8FL65	MURD_ECOL6 UDP-N-acetylmuramoylalanine--D-glutamate li...	352	7e-96
<input type="checkbox"/>	sp Q8X9Y9	MURD_ECO57 UDP-N-acetylmuramoylalanine--D-glutamate li...	352	7e-96
<input type="checkbox"/>	tr Q83MF9	UDP-N-acetylmuramoylalanine-D-glutamate ligase [MURD] ...	351	2e-95

<input type="checkbox"/>	tr Q7UDS6	UDP-N-acetylmuramoylalanine-D-glutamate ligase [MURD] ...	349	6e-95
<input type="checkbox"/>	sp Q8ZIF1	MURD_YERPE UDP-N-acetylmuramoylalanine--D-glutamate li...	347	2e-94
<input type="checkbox"/>	sp Q8E9P6	MURD_SHEON UDP-N-acetylmuramoylalanine--D-glutamate li...	344	1e-93
<input type="checkbox"/>	tr Q7N145	UDP-N-acetylmuramoylalanine--D-glutamate ligase (UDP-N...	332	8e-90
<input type="checkbox"/>	tr Q82VS5	UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3...	329	6e-89
<input type="checkbox"/>	sp Q9F1N2	MURD_SHEVI UDP-N-acetylmuramoylalanine--D-glutamate li...	320	2e-86
<input type="checkbox"/>	sp P45063	MURD_HAEIN UDP-N-acetylmuramoylalanine--D-glutamate li...	317	3e-85
<input type="checkbox"/>	sp Q8DEK8	MURD_VIBVU UDP-N-acetylmuramoylalanine--D-glutamate li...	315	1e-84
<input type="checkbox"/>	sp Q87SG6	MURD_VIBPA UDP-N-acetylmuramoylalanine--D-glutamate li...	315	1e-84
<input type="checkbox"/>	tr Q7NPZ7	UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3...	314	2e-84
<input type="checkbox"/>	tr Q7MNV3	UDP-N-acetylmuramoylalanine-D-glutamate ligase [VV0612...	313	3e-84
<input type="checkbox"/>	tr Q7VP56	UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]...	311	1e-83
<input type="checkbox"/>	sp Q9CPB0	MURD_PASMU UDP-N-acetylmuramoylalanine--D-glutamate li...	301	2e-80
<input type="checkbox"/>	sp Q9KPG5	MURD_VIBCH UDP-N-acetylmuramoylalanine--D-glutamate li...	299	5e-80
<input type="checkbox"/>	sp Q8XVI5	MURD_RALSO UDP-N-acetylmuramoylalanine--D-glutamate li...	298	2e-79
<input type="checkbox"/>	tr Q7VQI9	UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase (EC ...	280	3e-74
<input type="checkbox"/>	sp Q8D2Z4	MURD_WIGBR UDP-N-acetylmuramoylalanine--D-glutamate li...	276	4e-73
<input type="checkbox"/>	tr Q7W4B2	Putative peptidoglycan synthesis protein [MURD] [Borde...	268	1e-70
<input type="checkbox"/>	tr Q7WFS0	Putative peptidoglycan synthesis protein [MURD] [Borde...	268	2e-70
<input type="checkbox"/>	sp P57313	MURD_BUCAI UDP-N-acetylmuramoylalanine--D-glutamate li...	263	6e-69
<input type="checkbox"/>	tr Q7VUQ1	Putative peptidoglycan synthesis protein [MURD] [Borde...	262	1e-68
<input type="checkbox"/>	sp Q89AQ2	MURD_BUCBP UDP-N-acetylmuramoylalanine--D-glutamate li...	252	1e-65
<input type="checkbox"/>	sp Q9JSZ5	MURD_NEIMA UDP-N-acetylmuramoylalanine--D-glutamate li...	250	3e-65
<input type="checkbox"/>	sp Q8R9G4	MURD_THETN UDP-N-acetylmuramoylalanine--D-glutamate li...	247	2e-64
<input type="checkbox"/>	sp Q9K0Y4	MURD_NEIMB UDP-N-acetylmuramoylalanine--D-glutamate li...	246	7e-64
<input type="checkbox"/>	sp Q8K9T2	MURD_BUCAP UDP-N-acetylmuramoylalanine--D-glutamate li...	242	1e-62
<input type="checkbox"/>	tn AAR36463	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC ...	234	2e-60
<input type="checkbox"/>	tr Q82AD8	Putative UDP-N-acetylmuramoylalanine-D-glutamate ligas...	214	3e-54
<input type="checkbox"/>	tn AAS42861	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC ...	207	2e-52
<input type="checkbox"/>	sp Q97RU8	MURD_STRPN UDP-N-acetylmuramoylalanine--D-glutamate li...	207	3e-52
<input type="checkbox"/>	sp Q9S2W9	MURD_STRCO UDP-N-acetylmuramoylalanine--D-glutamate li...	207	3e-52
<input type="checkbox"/>	tr Q819Q2	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6....	206	6e-52
<input type="checkbox"/>	tr Q9ZHB0	D-glutamic acid adding enzyme MurD [MURD] [Streptococc...	206	8e-52
<input type="checkbox"/>	tr Q81WC9	UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]...	205	1e-51
<input type="checkbox"/>	sp Q8DQM2	MURD_STRR6 UDP-N-acetylmuramoylalanine--D-glutamate li...	204	2e-51
<input type="checkbox"/>	sp Q03522	MURD_BACSU UDP-N-acetylmuramoylalanine--D-glutamate li...	202	1e-50
<input type="checkbox"/>	sp Q9K9S8	MURD_BACHD UDP-N-acetylmuramoylalanine--D-glutamate li...	201	3e-50
<input type="checkbox"/>	tn CAE80955	MurD protein (EC 6.3.2.9) [MURD] [Bdellovibrio bacte...	198	1e-49
<input type="checkbox"/>	sp Q8KGD2	MURD_CHLTE UDP-N-acetylmuramoylalanine--D-glutamate li...	196	6e-49
<input type="checkbox"/>	sp Q8UDM6	MURD_AGRT5 UDP-N-acetylmuramoylalanine--D-glutamate li...	190	4e-47
<input type="checkbox"/>	tr Q7NEZ5	UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]...	190	5e-47
<input type="checkbox"/>	sp Q8DMN8	MURD_SYNEL UDP-N-acetylmuramoylalanine--D-glutamate li...	189	1e-46
<input type="checkbox"/>	sp Q9A597	MURD_CAUCR UDP-N-acetylmuramoylalanine--D-glutamate li...	187	3e-46
<input type="checkbox"/>	sp Q8E6P1	MURD_STRA3 UDP-N-acetylmuramoylalanine--D-glutamate li...	184	3e-45
<input type="checkbox"/>	tr Q8A256	UDP-N-acetylmuramoylalanine--D-glutamate ligase [BT345...	183	4e-45

<input type="checkbox"/>	sp	Q8E186	MURD_STRA5 UDP-N-acetylmuramoylalanine--D-glutamate li...	182	1e-44
<input type="checkbox"/>	sp	Q8ER50	MURD_OCEIH UDP-N-acetylmuramoylalanine--D-glutamate li...	180	4e-44
<input type="checkbox"/>	sp	Q8YI68	MURD_BRUME UDP-N-acetylmuramoylalanine--D-glutamate li...	179	6e-44
<input type="checkbox"/>	sp	Q8FZP2	MURD_BRUSU UDP-N-acetylmuramoylalanine--D-glutamate li...	179	8e-44
<input type="checkbox"/>	sp	Q8DVE3	MURD_STRMU UDP-N-acetylmuramoylalanine--D-glutamate li...	177	2e-43
<input type="checkbox"/>	sp	Q97EB9	MURD_CLOAB UDP-N-acetylmuramoylalanine--D-glutamate li...	177	3e-43
<input type="checkbox"/>	sp	Q9CF91	MURD_LACLA UDP-N-acetylmuramoylalanine--D-glutamate li...	176	5e-43
<input type="checkbox"/>	sp	O07669	MURD_ENTHR UDP-N-acetylmuramoylalanine--D-glutamate li...	176	7e-43
<input type="checkbox"/>	sp	O06222	MURD_MYCTU UDP-N-acetylmuramoylalanine--D-glutamate li...	175	1e-42
<input type="checkbox"/>	sp	O68388	MURD_STRPY UDP-N-acetylmuramoylalanine--D-glutamate li...	175	2e-42
<input type="checkbox"/>	tr	Q879A1	Putative UDP-N-acetylmuramoylalanine-D-glutamate [SPS0...	175	2e-42
<input type="checkbox"/>	sp	Q8P063	MURD_STRP8 UDP-N-acetylmuramoylalanine--D-glutamate li...	174	2e-42
<input type="checkbox"/>	sp	Q8XHM4	MURD_CLOPE UDP-N-acetylmuramoylalanine--D-glutamate li...	174	2e-42
<input type="checkbox"/>	tr	Q899G5	UDP-N-acetylmuramoylalanine-d-glutamate ligase (EC 6.3...	174	3e-42
<input type="checkbox"/>	tr	Q7VEP7	UDP-N-acetylmuramoylalanine-D-glutamate ligase MurD (E...	174	3e-42
<input type="checkbox"/>	sp	O67852	MURD_AQUAE UDP-N-acetylmuramoylalanine--D-glutamate li...	173	4e-42
<input type="checkbox"/>	sp	O07108	MURD_ENTFA UDP-N-acetylmuramoylalanine--D-glutamate li...	173	6e-42
<input type="checkbox"/>	tr	Q7MWM5	UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]...	173	6e-42
<input type="checkbox"/>	tr	Q89FU5	UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]...	169	8e-41
<input type="checkbox"/>	sp	Q8CSX6	MURD_STAEP UDP-N-acetylmuramoylalanine--D-glutamate li...	168	1e-40
<input type="checkbox"/>	sp	Q52953	MURD_RHIME UDP-N-acetylmuramoylalanine--D-glutamate li...	168	2e-40
<input type="checkbox"/>	sp	O33595	MURD_STAAM UDP-N-acetylmuramoylalanine--D-glutamate li...	167	3e-40
<input type="checkbox"/>	sp	Q8NX35	MURD_STAAW UDP-N-acetylmuramoylalanine--D-glutamate li...	167	4e-40
<input type="checkbox"/>	tn	AAS04216	MurD [MURD] [Mycobacterium paratuberculosis]	166	5e-40
<input type="checkbox"/>	sp	Q98KB1	MURD_RHILO UDP-N-acetylmuramoylalanine--D-glutamate li...	164	3e-39
<input type="checkbox"/>	sp	P57995	MURD_MYCLE UDP-N-acetylmuramoylalanine--D-glutamate li...	163	5e-39
<input type="checkbox"/>	sp	Q8YPS9	MURD_ANASP UDP-N-acetylmuramoylalanine--D-glutamate li...	163	5e-39
<input type="checkbox"/>	sp	Q88V80	MURD_LACPL UDP-N-acetylmuramoylalanine--D-glutamate li...	163	6e-39
<input type="checkbox"/>	tn	CAE28973	UDP-N-acetylmuramoylalanine-D-glutamate ligase precu...	160	4e-38
<input type="checkbox"/>	sp	Q8FNT8	MURD_COREF UDP-N-acetylmuramoylalanine--D-glutamate li...	159	1e-37
<input type="checkbox"/>	tr	Q7U8T1	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6....	157	4e-37
<input type="checkbox"/>	sp	Q929Y1	MURD_LISIN UDP-N-acetylmuramoylalanine--D-glutamate li...	156	6e-37
<input type="checkbox"/>	sp	Q8Y5M1	MURD_LISMO UDP-N-acetylmuramoylalanine--D-glutamate li...	155	1e-36
<input type="checkbox"/>	sp	Q9ZDC2	MURD_RICPR UDP-N-acetylmuramoylalanine--D-glutamate li...	155	1e-36
<input type="checkbox"/>	tn	CAF20500	UDP-N-ACETYLMURAMOYLALANINE D-GLUTAMATE LIGASE (EC 6...	153	5e-36
<input type="checkbox"/>	sp	Q821S1	MURD_CHLCV UDP-N-acetylmuramoylalanine--D-glutamate li...	152	8e-36
<input type="checkbox"/>	sp	P73668	MURD_SYNY3 UDP-N-acetylmuramoylalanine--D-glutamate li...	152	1e-35
<input type="checkbox"/>	tn	CAE50125	Putative UDP-N-acetylmuramoylalanine-D-glutamate lig...	150	5e-35
<input type="checkbox"/>	tn	AAS08792	UDP-N-acetylmuramoylalanine--D-glutamate ligase [LJ0...	149	7e-35
<input type="checkbox"/>	tn	CAE77734	MurD protein (EC 6.3.2.9) [MURD] [Bdellovibrio bacte...	148	2e-34
<input type="checkbox"/>	tr	Q7V5V5	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6....	147	3e-34
<input type="checkbox"/>	sp	Q8G4Q6	MURD_BIFLO UDP-N-acetylmuramoylalanine--D-glutamate li...	147	4e-34
<input type="checkbox"/>	sp	Q9RRJ4	MURD_DEIRA UDP-N-acetylmuramoylalanine--D-glutamate li...	145	1e-33
<input type="checkbox"/>	sp	Q8F7V4	MURD_LEPIN UDP-N-acetylmuramoylalanine--D-glutamate li...	143	6e-33
<input type="checkbox"/>	tr	Q83HK0	UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]...	142	8e-33

Graphical overview of the alignments[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs

([?](#) Help) (use ScanProsite for more details about PROSITE matches)



Submission	Matches on query sequence		Mat
	1	50 100 150 200 250 300 350 400	
MURD_PSEAE			
MURD_PSESM			
MURD_PSEPK			
Q83F28			
MURD_SALTY			
MURD_SALTI			
MURD_ECOLI			
MURD_ECOL6			
MURD_EC057			
Q83MF9			
Q7UDS6			
MURD_YERPE			
MURD_SHEON			
Q7N145			
Q82VS5			
MURD_SHEVI			
MURD_HAEIN			
MURD_VIBVU			
MURD_VIBPA			
Q7NPZ7			
Q7MNV3			
Q7VP56			
MURD_PASMU			
MURD_VIBCH			
MURD_RAL50			
Q7VQI9			
MURD_HIGBR			
Q7H4B2			
Q7HFS8			
MURD_BUCAI			
Q7VUQ1			
MURD_BUCBP			
MURD_NEIMA			
MURD_THETN			
MURD_NEIMB			
MURD_BUCAP			
AAR36463			
Q82AD8			
AAS42861			
MURD_STRPN			
MURD_STRCO			
Q819Q2			
Q9ZH88			
Q81WC9			
MURD_STRR6			
MURD_BACSU			
MURD_BACHD			
CAE88955			
MURD_CHLTE			
MURD_AGR75			
Q7NEZ5			
MURD_SYNEL			
MURD_CAUCR			
MURD_STRA3			
Q8A256			
MURD_STRA5			
MURD_OCETH			
MURD_BRUME			
MURD_BRUSU			
MURD_STRMU			
MURD_CLOAB			
MURD_LACLA			
MURD_ENTHR			
MURD_MYCTU			
MURD_STRPY			
Q879A1			
MURD_STRP8			
MURD_CLOPE			
Q899G5			
Q7VEP7			
MURD_AQUAE			
MURD_ENTFA			
Q7MMH5			
Q89FU5			
MURD_STAEP			
MURD_RHIME			
MURD_STAAM			
MURD_STAAM			
AAS84216			
MURD_RHIL0			
MURD_MYCLE			
MURD_ANASP			
MURD_LACPL			
CAE28973			
MURD_COREF			
Q7U8T1			
MURD_LACPL			

Alignments

sp Q9HVZ9 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 448
MURD_PSEAE 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Pseudomonas
aeruginosa]

Score = 839 bits (2167), Expect = 0.0

Identities = 429/448 (95%), Positives = 429/448 (95%)

Query: 1 MSLIASDHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCG 60
MSLIASDHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCG
Sbjct: 1 MSLIASDHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCG 60

Query: 61 ELDAEFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAK 120
ELDAEFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAK
Sbjct: 61 ELDAEFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAK 120

Query: 121 STVTTLVGEMAVAADKRVAVGGNLTGPALDLLADDIELYVLELSSFQLETCDRLNAEVAT 180
STVTTLVGEMAVAADKRVAVGGNLTGPALDLLADDIELYVLELSSFQLETCDRLNAEVAT
Sbjct: 121 STVTTLVGEMAVAADKRVAVGGNLTGPALDLLADDIELYVLELSSFQLETCDRLNAEVAT 180

Query: 181 VLNVEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPD 240
VLNVEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPD
Sbjct: 181 VLNVEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPD 240

Query: 241 FKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
FKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSN GHAVGLPFDAMLGAL
Sbjct: 241 FKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNALAALALGHAVGLPFDAMLGAL 300

Query: 301 KAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
KAFSGLAHRCQWVRERQGVSYDDSKATNV DIDGKLVLLAGGDGKGAD
Sbjct: 301 KAFSGLAHRCQWVRERQGVSYDDSKATNVGAALAAIEGLGADIDGKLVLLAGGDGKGAD 360

Query: 361 FHDLREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAELAREGDAVLL 420
FHDLREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAELAREGDAVLL
Sbjct: 361 FHDLREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAELAREGDAVLL 420

Query: 421 SPACASLDMFKNFEERGRLFAKAVEELA 448
SPACASLDMFKNFEERGRLFAKAVEELA
Sbjct: 421 SPACASLDMFKNFEERGRLFAKAVEELA 448

sp Q87WY3 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 448
MURD_PSESM 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Pseudomonas
syringae (pv. tomato)]

Score = 676 bits (1743), Expect = 0.0

Identities = 336/448 (75%), Positives = 381/448 (85%)

Query: 1 MSLIASDHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCG 60
MSLI SD FRIVVGLGKSGMSLVR+LA RG+ FAV DTRENPPELATLR YPQVEVRCG

Sbjct: 1 MSLIVSDRFRIVVGLGKSGMSLVRLANRGVSFAVADTRENPPPELATLRRDYPQVEVRCG 60

Query: 61 ELDAEFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAK 120
ELD +FLC A ELYVSPGL+L TPAL QA A+G ++SGDI+LFAR AKAP++AITGSNAK

Sbjct: 61 ELDVDFLCRADELYVSPGLALATPALQQAARGAKLSGDIELFARYAKAPVIAITGSNAK 120

Query: 121 STVTTLVGEMAVAADKRVAVGGNLTGTPALDLLADDIELYVLELSSSFQLETCDRLNAEVAT 180
STVTTLVGEMA AA KRVAVGGNLTGTPALDLL+DD+ELYV+ELSSSFQLET D+LNAEVAT

Sbjct: 121 STVTTLVGEMAAAAGKRVAVGGNLTGTPALDLLSDDVELYVMELSSSFQLETTDQLNAEVAT 180

Query: 181 VLNVEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKP 240
VLN+SEDHMDRY G+ YHLAKHRIFRGARQVVVNR DAL+RPLI + +PCW+FGLNKP

Sbjct: 181 VLNISEDHMDRYSGLPAYHLAKHRIFRGARQVVVNRQDALSRPLIGEGLPCWTFGLNKP 240

Query: 241 FKAFLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXGHAVGLPFDAMLGAL 300
F FGL EE+G+K+LAFQF+ L+PV ELK+RGAHN +N GHAVGLPFDAML +L

Sbjct: 241 FHGFLREENGEKFLAFQFENLMPVSELKVRGAHNQANALALALGHAVGLPFDAMLSSL 300

Query: 301 KAFSGLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
+ F+GL HRCQW+RER GV YY+DSKATNV DI GKLVL+AGGDGKGAD

Sbjct: 301 REFTGLEHRCQWLRERNGVDYNDKATNVGAALAAIEGLGSDIGGKLVLIAGGDGKGAD 360

Query: 361 FHDLPREPVARFCRAVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDAVLL 420
F LR PVA++CRA VLLGRDA LIAQALG+AVPL+RV T+ A ++AELA+ GDAVLL

Sbjct: 361 FSGLRAPVAKYCRAAVLLGRDAELIAQALGDAVPLIRVDTVQAAAERSAELAQRGDAVLL 420

Query: 421 SPACASLDMFKNFEERGRLEFAKAVEELA 448
SPACASLDMFKN+EERGR+FA+AVE L+

Sbjct: 421 SPACASLDMFKNYEERGRVFAQAVECLS 448

sp Q88N78 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 450
MURD_PSEPK 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Pseudomonas
putida (strain KT2440)]

Score = 675 bits (1742), Expect = 0.0
Identities = 343/448 (76%), Positives = 378/448 (83%)

Query: 1 MSLIASDHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPPELATLRAQYPQVEVRCG 60
+SLIASD FRIVVGLGKSGMSLVRLA RG+ FAV DTRE PPEL TLR YPQVEVRCG

Sbjct: 3 VSLIASDQFRIVVGLGKSGMSLVRLASRGIAFAVADTREQPPPELETTLRRDYPQVEVRCG 62

Query: 61 ELDAEFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAK 120
ELD +FLC A ELYVSPGL+L TPAL QAAA+GV++SGDI+LFAR AKAPIVAI+GSNAK

Sbjct: 63 ELDVDFLCRANELYVSPGLALATPALQQAARGVKLSGDIELFARHAKAPIVAISGSNAK 122

Query: 121 STVTTLVGEMAVAADKRVAVGGNLTGTPALDLLADDIELYVLELSSSFQLETCDRLNAEVAT 180
STVTTLVGEMA A KRVAVGGNLTGTPALDLLADDIELYVLELSSSFQLET D+LNAEVAT

Sbjct: 123 STVTTLVGEMAAKAGKRVAVGGNLTGTPALDLLADDIELYVLELSSSFQLETTDQLNAEVAT 182

Query: 181 VLNVEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKP 240
VLN+SEDHMDRY G+ YHLAKHRIFRGARQVVVNR DAL+RPL + PCW+FGLN PD

Sbjct: 183 VLNISEDHMDRYSGLPAYHLAKHRIFRGARQVVVNRQDALSRPLPVEGRPCWTFGLNPPD 242

Query: 241 FKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
 FKAFGL E DG+K+LAF+F L+P ELK+RGHN SN GHA GLPF+ ML AL
 Sbjct: 243 FKAFGLREVVDGEKYLAQFEFQTLMPARELKVIRGAHNQSNALALALGHAAGLPFPEPMLEAL 302

Query: 301 KAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
 + F GLAHRCQWVRER GV++YDDSKATNV DI+GKLVLL+AGGDGKGA+
 Sbjct: 303 REFGLAHRCQWVRERNGVNWYDDSKATNVGAALAAIEGLGADIEGKLVLIAGGDGKGAE 362

Query: 361 FHDLREPVARFCRAVVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDAVLL 420
 F LREPV RFCRAVVLLGRDA +A+ALG+AVPLVRV TLD+AV+Q AELA+ GDAVLL
 Sbjct: 363 FTALREPVKRFCRAVVLLGRDAERLAEALGDAVPLVRVKTLDQVQCAELAQAAGDAVLL 422

Query: 421 SPACASLDMFKNFEERGRLFAKAVEELA 448
 SPACASLDMFKNFEERGRLFA+A LA
 Sbjct: 423 SPACASLDMFKNFEERGRLFAQAAGGLA 450

tr Q83F20 UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD] 442
 [Coxiella
 burnetii] AA
align

Score = 365 bits (938), Expect = e-100
 Identities = 194/445 (43%), Positives = 280/445 (62%), Gaps = 4/445 (0%)

Query: 4 IASDHFRIVVGLGKSGMSLVRYLARRGLPFAVDTRENPPPELATLRAQYPQVEVRCGELD 63
 ++S+ ++VGLGK+G+S ++LA + PFAV+D+RE PPE YP+VE+ G+
 Sbjct: 1 MSSESLTVIVVGLGKTGLSQAQFLAAKNQFAVMDSREEPEWENFIKTYPRVELIRGQFS 60

Query: 64 AEFLCSARELYVSPGLSLRTPALVQAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTV 123
 + L A+E+ +SPG+SL+ P + + AA+G I GDI+LFAR PI+AITGSN K+TV
 Sbjct: 61 EKLLNEAQEIILSPGVSLQEPLIAKQAAQKSIIGDIELFARNVKNPIIAITGSNGKTTV 120

Query: 124 TTLVGEMAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLN 183
 TT+VG M AA + V+V GN+G P L+ + + YVLELSSFQLET L ++ AT+LN
 Sbjct: 121 TTVVGLMMKAAGRNVSVCGNIGEPVLEQITPEPDYVLELSSFQLETTFSLRSQAATILN 180

Query: 184 VSEDHMDRYDGMADYHLAKHRIFRGARQVVNRAD-ALTRPLIADTVPCWSFGLNKPDPFK 242
 +SEDHM+RY + DY AK RI+ +VN + + R L + P SFGLN +
 Sbjct: 181 ISEDHMNRYATLQDYLRAKQRIYTDCFIPIVNADEPEIWRHLFPNKKPL-SFGLN--NAA 237

Query: 243 AFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKA 302
 F L E + + +A+Q L+P+ ELK+ H+ N G A +P + ML L+
 Sbjct: 238 DFSLAEHNQKTSIAYQGKILMPIQELKLNARHHLQNALAALALGTAAKIPIENMLHVLRLD 297

Query: 303 FSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFH 362
 FSG+ HRCQWVR+ + + YY+DSK TNV G+L+L+AGG GKGADF
 Sbjct: 298 FSGIRHRCQWVRKYKEIDYNDKGTNVGATRAAIESLGQAAGQQLILIAGGQKGADFS 357

Query: 363 DLREPVARFCRAVVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDAVLLSP 422
 L++ V R+ + V+L+G DA L+ + L + +++EAV+++ + A+ GD VLLSP
 Sbjct: 358 PLKDVVKRYVKQVILIGEDAPLLEKTLKEITVIKHADSMNEAVKRSTQAAKAGDIVLLSP 417

Query: 423 ACASLDMFKNFEERGRLFAKAVEEL 447
 ACAS DMF N+E RG +F + VE L
 Sbjct: 418 ACASFDMFTNYEHRGDVFTETVEAL 442

sp Q8ZRU4 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 437**
 MURD_SALTY **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Salmonella
typhimurium]

Score = 354 bits (909), Expect = 1e-96
 Identities = 214/438 (48%), Positives = 268/438 (60%), Gaps = 11/438 (2%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +++GLG +G+S V + RG+ V+DTR PP L L + VE G L+ E+L +A
 Sbjct: 9 VIIGLGLTGLSCVDFFLARGVTPRVMDTRVTPPGLDKLPQE---VERHVGGLNDEWLLAA 65

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
 + SPG++L P+L AA+ GV I GDI+LF REA+APIVAITGSN KSTVTTLVGEM
 Sbjct: 66 DLIVASPGIALAHPSLSAAASAGVEIVGDIELFCREAQAPIVAITGSNGKSTVTTLVGEM 125

Query: 131 AVAADKRVAVGGNLGTPLDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHMD 190
 A AA V VGGN+G PAL LL D ELYVLELSSSFQLET L A ATVLNV+EDHMD
 Sbjct: 126 AKAAGVNVGVGGNIGLPALMLLDADRELYVLELSSSFQLETTSSLQAAAATVLNVTEDHMD 185

Query: 191 RYD-GMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKFAFGLIEE 249
 RY G+ Y AK R++ A+ VVN DALT P+ C SFG+N D+ L +
 Sbjct: 186 RYPFGLQOYRAAKLRVYEKAKVCVNNADALTMPVRGADERCVSFGVNMGDYH--LNRQ 242

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
 G+ WL + +K+L V E+K+ G HNY+N AVGLP + L AL F+GLAHR
 Sbjct: 243 QGETWLRVKGEKVLNVKEMKLSGQHNYTNALALADAVGLPRASSLKALTTFTGLAHR 302

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLPREPVA 369
 Q E GV + +DSKATNV +DG L LL GGDGK ADF L +
 Sbjct: 303 FQLALEHNGVRWINDSKATNV--GSTAALNGLHVDGTLHLLLGGDGKSADFSPLTRYLT 360

Query: 370 RFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACASLDM 429
 + GRD +A AL + + T++EA+R A + GD VLLSPACASLD
 Sbjct: 361 GDRIRLYCFGRDGAQLA-ALRPEI-AQQTETMEEAMRLLAPRVQPGDMVLLSPACASLDQ 418

Query: 430 FKNFEERGRLFAKAVEEL 447
 FKNFE+RG +F + +EL
 Sbjct: 419 FKNFEQRGDVFTRLAKEL 436

sp Q8Z9H0 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 437**
 MURD_SALTI **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Salmonella
typhi]

Score = 354 bits (909), Expect = 1e-96
 Identities = 216/442 (48%), Positives = 271/442 (60%), Gaps = 19/442 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +++GLG +G+S V + RG+ V+DTR PP L L + VE G L+ E+L +A
 Sbjct: 9 VIIGLGLTGLSCVDFFLARGVTPRVMDTRVTPPGLDKLPQE---VERHVGGLNDEWLLAA 65

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ SPG++L P+L AA+ GV I GDI+LF REA+APIVAITGSN KSTVTTLVGEM
Sbjct: 66 DLIVASPGIALAHPSLSAAASAGVEIVGDIELFCREAQAPIVAITGSNGKSTVTTLVGEM 125

Query: 131 AVAADKRVAVGGNLGTALDILLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEHDMD 190
A AA V VGGN+G PAL LL D ELYVLELSSSFQLET L A ATVLNV+EDHMD
Sbjct: 126 AKAAGVNVGVGGNIGLPALMLLDADRELYVLELSSSFQLETTSSLQAAAATVLNVTEHDMD 185

Query: 191 RYD-GMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDKAFGLIEE 249
RY G+ Y AK R++ A+ VVN DALT P+ C SFG+N D+ L +
Sbjct: 186 RYPFGLQQYRAAKLRVYEKAKVCVVNADALTMPVRGADERCVSFGVNMGDYH---LNRQ 242

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
G+ WL + +K+L V E+K+ G HNY+N AVGLP + L AL F+GLAHR
Sbjct: 243 QGETWLRVKGEKVLNVKEMKLSGQHNYTNALALADAVGLPRASSLKALTTFTGLAHR 302

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXXIDGKLVLLAGGDGKGADFHDLPVPA 369
Q E GV + +DSKATNV +DG L LL GGDGK ADF P+A
Sbjct: 303 FQLALEHNGVRWINDSKATNV--GSTAALNGLHVDGTLHLLGGDGKSADF----SPLA 356

Query: 370 RFCRA----VLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAELAREGDAVLLSPACA 425
R+ + GRD +A AL + + T++EA+R A + GD VLLSPACA
Sbjct: 357 RYLTGDRIRLYCFGRDGAQLA-ALRPEI-AQQTETMEEAMRLLAPHVQPGDMVLLSPACA 414

Query: 426 SLD MFKNFEERGRLFAKAVEEL 447
SLD FKNFE+RG +F + +EL
Sbjct: 415 SLDQFKNFEQRGDVFTRLAKEL 436

sp P14900 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 437**
MURD_ECOLI **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Escherichia
coli]

Score = 353 bits (905), Expect = 4e-96

Identities = 214/442 (48%), Positives = 269/442 (60%), Gaps = 19/442 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+++GLG +G+S V + RG+ V+DTR PP L L VE G L+ E+L +A
Sbjct: 9 VIIGLGLTGLSCVDFFLARGVTPRVM DTRMTPPGLDKLPEA---VERHTGSLNDEWLMAA 65

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ SPG++L P+L AA G+ I GDI+LF REA+APIVAITGSN KSTVTTLVGEM
Sbjct: 66 DLIVASPGIALAHPSLSAAADAGIEIVGDIELFCREAQAPIVAITGSNGKSTVTTLVGEM 125

Query: 131 AVAADKRVAVGGNLGTALDILLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEHDMD 190
A AA V VGGN+G PAL LL D+ ELYVLELSSSFQLET L A AT+LNV+EDHMD
Sbjct: 126 AKAAGVNVGVGGNIGLPALMLLDDECELYVLELSSSFQLETTSSLQAVAATILNVTEHDMD 185

Query: 191 RYD-GMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDKAFGLIEE 249
RY G+ Y AK RI+ A+ VVN DALT P+ C SFG+N D+ L +
Sbjct: 186 RYPFGLQQYRAAKLRIYENAKVCVVNADALTMPIRGADERCVSFGVNMGDYH---LNHQ 242

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
G+ WL + +K+L V E+K+ G HNY+N A GLP + L AL F+GL HR

Sbjct: 243 QGETWLRVKGEKVLNVKEMKLSGQHNYTNALALADAAGLPRASSLKALTTFTGLPHR 302

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPVA 369
+ V E GV + +DSKATNV +DG L LL GGDGK ADF P+A

Sbjct: 303 FEVVLEHNGVRWINDSKATNV--GSTAALNGLHVDGTLHLLLGGDGKSADF----SPLA 356

Query: 370 RFCRA---VLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACA 425
R+ + GRD +A AL V + T+++A+R A + GD VLLSPACA

Sbjct: 357 RYLNGDNVRLYCFGRDGAQLA-ALRPEV-AEQTETMEQAMRLLAPRVQPGDMVLLSPACA 414

Query: 426 SLDMFKNFEERGRLFAKAVEEL 447
SLD FKNFE+RG FA+ +EL

Sbjct: 415 SLDQFKNFEQRGNEFARLAKEL 436

sp Q8FL65 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 437
MURD_ECOL6 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Escherichia coli
06]

Score = 352 bits (903), Expect = 7e-96
Identities = 214/442 (48%), Positives = 269/442 (60%), Gaps = 19/442 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+++GLG +G+S V + RG+ V+DTR PP L L VE G L+ E+L +A

Sbjct: 9 VIIGLGLTGLSCVDFFLARGVTPRVMDTRMTPPGLDKLPEA---VERHTGGLNDEWLMAA 65

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ SPG++L P+L AA G+ I GDI+LF REA+APIVAITGSN KSTVTTLVGEM

Sbjct: 66 DLIVASPGIALAHPSLSAAADAGIEIVGDIELFCREAQAPIVAITGSNGKSTVTTLVGEM 125

Query: 131 AVAADKRVAVGGNLTGPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDHMD 190
A AA V VGGN+G PAL LL D+ ELYVLELSSFQLET L A AT+LNV+EDHMD

Sbjct: 126 AKAAGVNVGVGGNIGLPALMLLDDECELYVLELSSFQLETTSSLQAVAATILNVTEHDHMD 185

Query: 191 RYD-GMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKAFGLIEE 249
RY G+ Y AK RI+ A+ VVN DALT P+ C SFG+N D+ L +

Sbjct: 186 RYPFGLQQYRAAKLRIYENAKVCVNNADALTMPIRGADERCVSFGVMNGDYH---LNHQ 242

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
G+ WL + +K+L V E+K+ G HNY+N A GLP + L AL F+GL HR

Sbjct: 243 QGETWLRVKGEKVLNVKEMKLSGQHNYTNALALADAAGLPRASSLKALTTFTGLPHR 302

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPVA 369
+ V E GV + +DSKATNV +DG L LL GGDGK ADF P+A

Sbjct: 303 FEVVLEHNGVRWVNDKATNV--GSTAALNGLHVDGTLHLLLGGDGKSADF----SPLA 356

Query: 370 RFCRA---VLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACA 425
R+ + GRD +A AL V + T+++A+R A + GD VLLSPACA

Sbjct: 357 RYLNGDNVRLYCFGRDGAQLA-ALRPEV-AEQTETMEQAMRLLATRVQPGDMVLLSPACA 414

Query: 426 SLDMFKNFEERGRLFAKAVEEL 447
SLD FKNFE+RG FA+ +EL

Sbjct: 415 SLDQFKNFEQRGNEFARLAKEL 436

sp Q8X9Y9 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 437
MURD_ECO57 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Escherichia coli
O157:H7]

Score = 352 bits (903), Expect = 7e-96
Identities = 214/442 (48%), Positives = 269/442 (60%), Gaps = 19/442 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+++GLG +G+S V + RG+ V+DTR PP L L VE G L+ E+L +A
Sbjct: 9 VIIGLGLTGLSCVDFFLARGVTPRVMDTRMTPPGLDKLPEA---VERHTGSLNDEWLMAA 65

Query: 71 RELVSPGSLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ SPG++L P+L AA G+ I GDI+LF REA+APIVAITGSN KSTVTTLVGEM
Sbjct: 66 DLIVASPGIALAHPSLSAAADAGIEIVGDIELFCREAQAPIVAITGSNGKSTVTTLVGEM 125

Query: 131 AVAADKRVAVGGNLGTLPALDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHMD 190
A AA V VGGN+G PAL LL D+ ELYVLELSSSFQLET L A AT+LNV+EDHMD
Sbjct: 126 AKAAGVNVGVGGNIGLPALMLLDDECELYVLELSSSFQLETTSSLQAVAATILNVTEDEHMD 185

Query: 191 RYD-GMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDKAFGLIEE 249
RY G+ Y AK RI+ A+ VVN DALT P+ C SFG+N D+ L +
Sbjct: 186 RYPFGLQQYRAAKLRIYENAKVCVVNADDALTMPIRGADERCVSFGVNMGDYH---LNHQ 242

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
G+ WL + +K+L V E+K+ G HNY+N A GLP + L AL F+GL HR
Sbjct: 243 QGETWLRVKGEKVLNVKEMKLSGQHNYTNALALADAAGLPRASSLKALTFTTGLPHR 302

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLPVPA 369
+ V E GV + +DSKATNV +DG L LL GGDGK ADF P+A
Sbjct: 303 FEVVLEHNGVRWINDSKATNV--GSTAALNGLHVDGTLHLLGGDGKSADF----SPLA 356

Query: 370 RFCRA----VVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDVLLSPACA 425
R+ + GRD G+ AL V + T+++A+R A + GD VLLSPACA
Sbjct: 357 RYLNGDNVRLYCFGRD-GVQLAALRPEV-AEQTETMEQAMRLLAPRVQPGDMVLLSPACA 414

Query: 426 SLDMFKNFEERGRLFAKAVEEL 447
SLD FKNFE+RG FA+ +EL
Sbjct: 415 SLDQFKNFEQRGNEFARLAKEL 436

tr Q83MF9 UDP-N-acetylmuramoylalanine-D-glutamate ligase [MURD] 438
[Shigella
flexneri] AA
align

Score = 351 bits (900), Expect = 2e-95
Identities = 213/442 (48%), Positives = 268/442 (60%), Gaps = 19/442 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+++GLG +G+S V + RG+ V+DTR PP L L VE G L+ E+L +A
Sbjct: 10 VIIGLGLTGLSCVDFFLARGVTPRVMDTRMTPPGLDKLPEA---VERHTGSLNDEWLMAA 66

Query: 71 RELVSPGSLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ SPG++L P+L AA G+ I GDI+LF REA+APIVAITGSN KSTVTTLVGEM

Sbjct: 67 DLIVASPGIALAHPSLSAAADAGIEIVGDIELFCREAQAPIVAITGSNGKSTVTTLVGEM 126

Query: 131 AVAADKRVAVGGNLGT PALDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHMD 190
A AA V VGGN+G PAL LL D+ ELYVLELSSSFQLET L A AT+LNV+EDHMD

Sbjct: 127 AKAAGVNVGVGGNIGLPALMLLDDECELYVLELSSSFQLETTSSLQAVAATILNVTEDHMD 186

Query: 191 RYD-GMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKAFGLIEE 249
RY G+ Y AK RI+ A+ VVN DALT P+ C SFG+N D+ L +

Sbjct: 187 RYPFGLQQYRAAKLRIYENAKVCVVNADALTMPIRGADERCVSFGVNMGDYH---LNHQ 243

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
G+ WL + +K+L V E+K+ G HNY+N A GLP + L AL F+GL HR

Sbjct: 244 QGETWLRVKGEKVLNVKEMKLSGQHNYTNALVALALADAAGLPRASSLKALTTFGLPHR 303

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPVA 369
+ V E GV + +DSKATNV +DG L LL GGDGK ADF P+

Sbjct: 304 FEVVLEHNGVRWINDSKATNV--GSTAALNGLHVDGTLHLLGGDGKSADF----SPLV 357

Query: 370 RFCRA----VLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAELAREGDAVLLSPACA 425
R+ + GRD +A AL V + T+++A+R A + GD VLLSPACA

Sbjct: 358 RYLNGDNVRLYCFGRDGAQLA-ALRPEV-AEQTETMEQAMRLAPRVQPGDMVLLSPACA 415

Query: 426 SLDMFKNFEERGRLFAKAVEEL 447
SLD FKNFE+RG FA+ +EL

Sbjct: 416 SLDQFKNFEQRGNEFARLAKEL 437

tr Q7UDS6 UDP-N-acetylmuramoylalanine-D-glutamate ligase [MURD] 438
[Shigella
flexneri] AA
align

Score = 349 bits (895), Expect = 6e-95
Identities = 213/442 (48%), Positives = 267/442 (60%), Gaps = 19/442 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+++GLG +G+S V + RG+ V+DTR PP L L VE G L+ E+L +A

Sbjct: 10 VIIGLGLTGLSCVDFFLARGVTPRVMDTRMTPPGLDKLPEA---VERHTGSLNDEWLMAA 66

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ SPG++L P+L AA G+ I GDI+LF REA+APIVAITGSN KSTVTTLVGEM

Sbjct: 67 DLIVASPGIALAHPSLSAAADAGIEIVGDIELFCREAQAPIVAITGSNGKSTVTTLVGEM 126

Query: 131 AVAADKRVAVGGNLGT PALDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHMD 190
A AA V VGGN+G PAL LL D+ ELYVLELSSSFQLET L A AT+LNV+EDHMD

Sbjct: 127 AKAAGVNVGVGGNIGLPALMLLDDECELYVLELSSSFQLETTSSLQAVAATILNVTEDHMD 186

Query: 191 RYD-GMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKAFGLIEE 249
RY G+ Y AK RI+ A+ VVN DALT P+ C SFG+N D L +

Sbjct: 187 RYPFGLQQYRAAKLRIYENAKVCVVNADALTMPIRGADERCVSFGVNMGDCH---LNHQ 243

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
G+ WL + +K+L V E+K+ G HNY+N A GLP + L AL F+GL HR

Sbjct: 244 QGETWLRVKGEKVLNVKEMKLSGQHNYTNALVALALADAAGLPRASSLKALTTFGLPHR 303

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPVA 369
+ V E GV + +DSKATNV +DG L LL GGDGK ADF P+

Sbjct: 304 FEVVLEHNGVRWINDSKATNV--GSTEAALNGLHVDGTLHLLLGGDGKSADF---SPLV 357

Query: 370 RFCRA----VLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDVLLSPACA 425
R+ + GRD +A AL V + T+++A+R A + GD VLLSPACA

Sbjct: 358 RYLNGDNVRLYCFGRDGAQLA-ALRPEV-AEQTETMEQAMRLLAPRVQPGDMVLLSPACA 415

Query: 426 SLDMPKFNFEERGRLFAKAVEEL 447
SLD FKNFE+RG FA+ +EL

Sbjct: 416 SLDQFKNFEQRGNEFARLAKEL 437

sp Q8ZIF1 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 438**
MURD_YERPE **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Yersinia pestis]

Score = 347 bits (890), Expect = 2e-94
Identities = 208/438 (47%), Positives = 263/438 (59%), Gaps = 11/438 (2%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+++GLG +G+S V + RG+ V+DTR NPP L L VE G+L+ E+L A

Sbjct: 10 VIIGLGLTGLSCVDFFIARGVTPRVMDTRINPPGLDQLPES---VEQHVGDLNQEWLLDA 66

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ VSPG++L PAL +AA GV I GDI+LF RE +AP+VAITGSN KSTVTTLVGEM

Sbjct: 67 DLIVVSPGMALAHPALSEAAEAGVEIIGDIELCRENQAPVVAITGSNGKSTVTTLVGEM 126

Query: 131 AVAADKRVAVGGNLGTPALDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHMD 190
A AA V GGN+G PAL LL D +L VLELSSSFQLET L A AT+LNV+EDH D

Sbjct: 127 AKAAGWSVGGGGNIGVPALTLLKQDNQLTVLELSSSFQLETHSLRASAATILNVTEDHTD 186

Query: 191 RYD-GMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKFAFLIEE 249
RY G+ Y AK R++ A+ VVN DALT P+ C SFG++ D+ L ++

Sbjct: 187 RYPLGLQOYRAAKLRVYENAKVCVNNADALTMPVRGADSRCSISFGVDVGDYH--LNKQ 243

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
G+ WL + +K+L E+K+ G HNY+N AVG+P + L AL FSGL HR

Sbjct: 244 QGEIWLVRVGEKVLN TREMKLSGRHNYTNALALALADAVGIPRASSLKALTTFSGLPHR 303

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLPVA 369
Q V ER GV + +DSKATNV +DG L LL GGDGK ADF L +

Sbjct: 304 FQLVLERHGVWINDSKATNV--GSTEAALDGLQVDGTLHLLLGGDGKSADFSGLTHFLQ 361

Query: 370 RFCRAVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDVLLSPACASLDM 429
V GRD G +A + L T+ +A+ A++ GD VLLSPACASLD

Sbjct: 362 GDRIKVYCFGRDGGQLAALRPDVSQLTE--TMAQAMALVAKVVLPGDRVLLSPACASLDQ 419

Query: 430 FKNFEERGRLFAKAVEEL 447
F++FE RG FA+ EEL

Sbjct: 420 FRSFEHRGNEFARLAEEL 437

sp Q8E9P6 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 439**
MURD_SHEON **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align

(D-glutamic acid adding enzyme) [MURD] [Shewanella
oneidensis]

Score = 344 bits (883), Expect = 1e-93

Identities = 191/445 (42%), Positives = 274/445 (60%), Gaps = 14/445 (3%)

Query: 6 SDHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAE 65
S + IV+GLG +G+S+VRYL +G+ V+D+R PP TL + +P+V++ G D
Sbjct: 3 SQYSHIVLGLGATGLSVVRYLCGKGITPLVMSRRQPPGAETLASSFPEVKLIAGGFDCR 62

Query: 66 FLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFARE---KAPIVAITGSNAKST 122
+L A ++ +SPG+++ TP + A G+ + GD++LFARE K ++ ITGSN K+T
Sbjct: 63 YLVQATQIIISPFIAMNTPEVRAALDMGIEVIGDVELFAREIADRKPCVIGITGSNGKTT 122

Query: 123 VTTLVGEMAVAADKRVAVGGNLTGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVL 182
VTTLVGEM A VAVGGN+G PALDLL ++ +++VLELSSFQLET LN +T L
Sbjct: 123 VTTLVGEMLRAGIAVAVGGNIGIPALDLLKENADIFVLELSSFQLETTTHSLNCAVASTCL 182

Query: 183 NVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRAADALTRPLIADTVPCWSFGLNKPDKF 242
NV+EDHMDRY M Y AK R++ +R ++ NR DALT P + + SFGL P+
Sbjct: 183 NVTEDHMDRYSDMDAYRKAKLRLYHQSRSIIFNRDDALTIP--TEPMNQNSFGLAPPEGD 240

Query: 243 AFGLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKA 302
+G+ + + +++P+ E+ + G+HN++N +AVG+ M +
Sbjct: 241 EWGICDSK---IYHGHSEIMPITEVSLIGSHNHANLLAAMALVYAVGVDKQVMANVART 296

Query: 303 FSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFH 362
F+GL+HRC+ V + GV+Y +DSKATNV + G ++L+AGGDGKGADF
Sbjct: 297 FTGLSHRCEVVGKGGVTYVNDKATNVGATVAALDGLSDHL-GDIILIAGGDGKGADFS 355

Query: 363 DLREPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSP 422
L EP+ + ++ LGRD IA A ++V ++ AV +AA+LA GD VLLSP
Sbjct: 356 PLEEPLTKVTH-LITLGRDGNKIAALKEGA---IKVDSMAAAVAKAAQLATSGDIVLLSP 411

Query: 423 ACASLDMFKNFEERGRLFAKAVEEL 447
ACASLDM+ NF RG F VE+L
Sbjct: 412 ACASLDMYSNFMARGDDFRSQVEQL 436

tr Q7N145 UDP-N-acetylmuramoylalanine--D-glutamate ligase 436 AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Photorhabdus
luminescens (subsp. laumondii)]

Score = 332 bits (851), Expect = 8e-90

Identities = 199/438 (45%), Positives = 258/438 (58%), Gaps = 13/438 (2%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+++GLG +G+S V + RG+ V+DTR PP L VE G L+A++L A
Sbjct: 10 VIIGLGLTGLSCVDFMARGVIPRMDTRTAPPKDKLP---DGVECHSGSLNADWLMDA 66

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ VSPG++L T L AA G+ I GDI+LF REA APIVAITGSN KSTVT+LVGEM
Sbjct: 67 DLIVVSPGIALATAVLQAAANAGIEIVGDIELFCREATAPIVAITGSNGKSTVTSLVGEM 126

Query: 131 AVAADKRVAVGGNLTGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDHMD 190
A AA+ +V VGGN+G PAL+LL +LYVLELSSFQLET LNA A VLNV+EDHMD

Sbjct: 127 AKAANWQVGVGGNIGLPALELLKKSCQLYVLELSSFQLETTYSLNATAAAVLNVTEHDMD 186

Query: 191 RY-DGMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDKAFGLIEE 249
RY G++ Y AK RI+ A++ +VN D LT P + C SFG++ D++ +

Sbjct: 187 RYPQGVVSQYRAAKLRIYHQAKRCIVNAQDPLTLPEMGMDSRCVSGVDCGDYQL-----D 241

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
+L LL E+K+ G HNY+N AVG+P +A L L + GL HR

Sbjct: 242 SENAFKLVHNQSLLATNEIKLTGRHNYANGLVALALADAVGIPREASLATLTVPGLDHR 301

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKADFHDLEPVA 369
Q R +GV + +DSKATNV +++G L LL GGDGK ADF L+ +

Sbjct: 302 FQLARLNKGVRWINDSKATNV--GSTMAALDGLNLEGTLYLLLGGDGKSADFSPKPFLLC 359

Query: 370 RFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACASLDM 429
+ GRD +AQ L T+++A+R A GD VLLSPACASLD

Sbjct: 360 GNKVQLYCFGRDGKQLAQLRPEIATLTE--TMEQAIRDIAPRLVAGDMVLLSPACASLDQ 417

Query: 430 FKNFEERGRLFAKAVEEL 447
F+NFE+RG F + EEL

Sbjct: 418 FRNFEQRGHEFTRLAEEL 435

tr Q82VS5 **UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9)** 471
[MURD] AA
[Nitrosomonas europaea] align

Score = 329 bits (843), Expect = 6e-89

Identities = 198/453 (43%), Positives = 267/453 (58%), Gaps = 24/453 (5%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+V+G+GK+G+S+V++L+R G +V DTR +PP L + P + CG L E

Sbjct: 9 LVLGMGKTGISMVKWLSRLGAQLSVADTRTSPPNLELISRIVPGEAIFCGPLKEELFQGI 68

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFA--REAKAP----IVAITGSNAKSTVT 124
+ +SPG+++ P + A +GV + GDI+LFA + AP I+AITGSN K+TVT

Sbjct: 69 DAIAISPGBVAEPLVQAAALQQGVPIVDIELFAVALDQYAPPGTKILAITGSNGKTTVT 128

Query: 125 TLVGEMAVAADKRVAVGGNLGTPALDLLADDIE-----LYVLELSSFQLETCDRNLNAEV 178
++VGEM A V V GN+G ALD L ++ L+ LELSSFQLET L +

Sbjct: 129 SMVGEMVKNAGWDVEVAGNIGPAALDALMQRMDANKWPHLWALELSSFQLETTSSLRPDA 188

Query: 179 ATVLNVSEHDMDRYDGMADYHLAKHRIF-----RGARQVVVNADALTRPLIADTVPCWS 233
ATVLN+SEDH+DRYD + +Y AK RIF G Q++ NR DA + +

Sbjct: 189 ATVLNLSHDHLDYDSIEEYAAAKARIFSRPHNNGCVQIL-NRDDARVYAMADKNSKQVT 247

Query: 234 FGLNKP-DFKAFLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLP 292
FGL+ P + FGL+ WLA LL EL + G HN +N AV LP

Sbjct: 248 FGLSAPVSDEEFGLLPGGSDVWLAQGSTHLLKTSELAVAGLHNAANALALCRAVDLP 307

Query: 293 FDAMLGALKAFSGLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLA 352
F+ +L AL+ F GL HR Q V E GV++YDDSK+TN+ ++ +L+A

Sbjct: 308 FEPLLHALRTFRGLPHRMQKVAEFNGVTYDDSKSTNIGSAVAALNGFRKNV----ILIA 363

Query: 353 GGDGKGADFHDLEPVARFCRAVVLLGRDAGLIAQAL-GNAVPLVRVATLDEAVRQAAEL 411
GGDGKG DF L +PV++ R+VVLLGRDA +AQA+ + VP+ RV T+DEAV+ + L

Sbjct: 364 GGDGKGQDFSPLEQPVSKHVRSVVLLGRDADKVAQAIQASNVPIHRVTMDEAVQVSFLL 423

Query: 412 AREGDAVLLSPACASLDMFKNFEERGRLFAKAV 444

A GD VLLSPACASLDMF N+ R +F AV

Sbjct: 424 AEHGDVVLLSPACASLDMFNYYIHRAEVFTAAV 456

sp Q9F1N2 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 449**
 MURD_SHEVI **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) **align**
(D-glutamic acid adding enzyme) [MURD] [Shewanella
violacea]

Score = 320 bits (821), Expect = 2e-86

Identities = 186/445 (41%), Positives = 270/445 (59%), Gaps = 14/445 (3%)

Query: 7 DHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEF 66

D+ +V+GLG +G+S+VRYL R+G+ V+D+R+ PP L ++P+V + G D +

Sbjct: 4 DNSHLVLGLGATGLSVVRYLCRQGITPLVMDSRDQPPGAEQLALEFPEVNLITGGFDCRY 63

Query: 67 LCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAK--AP-IVAITGSNAKSTV 123

L A ++ +SPG+++ TP + A + + GD++LFAR K +P ++ ITGSN KSTV

Sbjct: 64 LVQASQIVISPGIAIDTPEIRAAIDMDIEVIGDVLELFARAIDKDRSPCVIGITGSNGKSTV 123

Query: 124 TTLVGEMAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLN 183

TTLVGEMA AA AVGGN+G P DLLL ++LY+LELSSFQLET LN AT LN

Sbjct: 124 TTLVGEMAKAAGLNYAVGGNIGIPVLDLLQKPVLDLYILELSSFQLETHSLNCISATCLN 183

Query: 184 VSEDHMDRYDGMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDFKA 243

+SEDHMDRY + Y AK ++ +++ + NR D+LT+P D + SFGL P

Sbjct: 184 ISEDHMDRYSDLEAYRQAKLALYDQSKRALFNREDSLTQP--NDPMNQNSFGLTSPVNDE 241

Query: 244 FGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAF 303

+G+ +DG+ + ++ + ++ I G+HN++N + G+ + M+ K F

Sbjct: 242 WGV--KD GK--IVHGTTEIASLQDVAIVGSHNHNALIAAMALAYHAGIDKEPMIQVAKNF 297

Query: 304 SGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHD 363

+GLAHRC+ V V+Y +DSKATNV + G ++L+ GGDGKGADF

Sbjct: 298 TGLAHRCELVANIAAVAYVNDKATNVGATVAALEGLGEHL-GDIILIVGGDGKGADFTP 356

Query: 364 LREPVARFCRAVVLLGRDAGLIAQALGNAPLVVRVATLDEAVRQAAELAREGDAVLLSPA 423

L E V ++ LG+D IA ++ + ++ +AV+QAAELA GD VLLSPA

Sbjct: 357 L-ETVFNKVAHLITLGKDGDKIAALKEHS---HKADSMADAVKQAAELATAGDIVLLSPA 412

Query: 424 CASLDMFKNFEERGRLFAKAVEELA 448

CASLDM+KNF RG F + + L+

Sbjct: 413 CASLDMYKNFMARGDDFRQLAQALS 437

sp P45063 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 437**
 MURD_HAEIN **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) **align**
(D-glutamic acid adding enzyme) [MURD] [Haemophilus
influenzae]

Score = 317 bits (811), Expect = 3e-85

Identities = 191/433 (44%), Positives = 252/433 (58%), Gaps = 18/433 (4%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSAR 71
 ++GLGK+G+S V YL + V+DTR+NP + L P + G L+ E+L +
 Sbjct: 11 IIGLGKTGLSCVDYLLSQANIRVIDTRKNPTGIDKLPQNIP---LHTGSLNQEWLLESD 67

Query: 72 ELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEMA 131
 + +SPGL+++TP + A GV + GDI+LF R A PIV ITGSN KSTVTTLV EMA
 Sbjct: 68 MIVISPLAVKTPEIQTALKAGVEVIGDIELFCRAATKPIVGITGSNGKSTVTTLVYEMA 127

Query: 132 VAADKRVAVGGNLGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDHMDR 191
 AA +V +GGN+G PAL LL +D ELYVLELSSFQLET L A ATVLNV+EDHMDR
 Sbjct: 128 KAAGVKVGMGGNIGIPALSLLNEDCELYVLELSSFQLETTYSLKAAAATVLNVTEDHMDR 187

Query: 192 YDGMADYHLAKHRIFRGARQVVVNRAALT---RPLIADTVPCWSFGLNKPDKAFGLI 247
 Y + DY AK RI+ A+ V+N D LT TV SF N D + L
 Sbjct: 188 YMDLEDYRQAKLRIYHNAKVGVLNEDRLTFGENENQAKHTV---SFAENSAD---YWLK 241

Query: 248 EEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLA 307
 E+G+++L + + +LP E + G HNY N A+G+ D++ AL+ F GL
 Sbjct: 242 TENGKQYLMVKDEVILPCEEATLVGRHNYMNILAATALAQAGINLDSIRTALRHFKGLD 301

Query: 308 HRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREP 367
 HR Q V + G+ + +DSKATNV I+GKL LL GGDGKGADF +L E
 Sbjct: 302 HRFQLVHQANGIRWINDSKATNVGSTVAALAGLY--IEGKLHLLGGDGKGADFSELAEL 359

Query: 368 VARFCRAVVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDAVLLSPACASL 427
 + + GRD L+A+ + T+++A+ + GD VLLSPACASL
 Sbjct: 360 INQPHIICYCFGRDGAALLAKFSSQS---YLFDTMEQAIEFLRPTLQSGDMVLLSPACASL 416

Query: 428 DMFKNFEERGRLF 440
 D F +FE+RG F
 Sbjct: 417 DQFASFEEKRGEEF 429

sp	<u>Q8DEK8</u>	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC	442
	MURD_VIBVU	6.3.2.9)	AA
		(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	<u>align</u>
		(D-glutamic acid adding enzyme) [MURD] [Vibrio	
		vulnificus]	

Score = 315 bits (806), Expect = 1e-84

Identities = 182/440 (41%), Positives = 248/440 (56%), Gaps = 10/440 (2%)

Query: 11 IVVGLGKSGMSLVRYLARRG--LPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLC 68
 +VVGLG +G+S+VR+L + L V+DTR PP + L P + + G + +L
 Sbjct: 11 VVVGLGITGLSVVRHLRKTQPQLQVKVIDTRPTPPGVEQLP---PDIALHVGSWNDAWLA 67

Query: 69 SARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVG 128
 A + +PG++L TP + A+GV + GDI+LFA A P++AITGSN KSTVT L G
 Sbjct: 68 EADLVVTNPGLALATPQIQTVLARGVAVVGDIELFAWAADKPVIAITGSNGKSTVTDLTG 127

Query: 129 EMAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDH 188
 MA A + A+GGN+G PALDLL ++ELYVLELSSFQLET L+ A LN+SEDH
 Sbjct: 128 VMANACGVKCAIGGNIGVPALDLLEQEVLYVLELSSFQLETTSSLHLVAAAFNLNSEDH 187

Query: 189 MDRYDGMADYHLAKHRIFRGARQVVVNRRADALTRPLIADTVPCWSFGLNKPDKAFGLIE 248
MDRY GM DY AK RIF+ A+ VVNR D T P + + D K FG+I
Sbjct: 188 MDRYQGMDDYRQAKLRIFQHAKHGVVNRDDRQTYPETSHGQQSLALVTFGSDDKEFGVIS 247

Query: 249 EDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAH 308
G+ WL++ +L ELK+ G HN +N G+ + L ALK+++GL H
Sbjct: 248 HQGESWLSYNQQPILASRELKLVGQHNVANVLVLLALTCAGIDYRKGLSALKSYTGLTH 307

Query: 309 RCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREP 368
RCQ V + +G+ + +DSKATN+ + GKL LL GGDGKGADF L+ +
Sbjct: 308 RCQVVADNRGIKWVNDKATNL--ASTQAALSGLNACGLYLLVGGDGKGADFSPLKPIL 365

Query: 369 ARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACASLD 428
A+ + G D +A R +++ + + + GD V+LSPACAS D
Sbjct: 366 AQLNLQLCCFGADGDQFMPLHASA---TRFERMEDVIEHISPQLQSGDMVMLSPACASFD 422

Query: 429 MFKNFEERGRLFAKAVEELA 448
F NF RG FA+ + A
Sbjct: 423 QFSNFMARGDRFAELARQYA 442

sp Q87SG6 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 437**
MURD_VIBPA **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) **align**
(D-glutamic acid adding enzyme) [MURD] [Vibrio
parahaemolyticus]

Score = 315 bits (806), Expect = 1e-84

Identities = 190/443 (42%), Positives = 253/443 (56%), Gaps = 15/443 (3%)

Query: 8 HFRIVVGLGKSGMSLVRYLARRG--LPFAVVDTRENPPELATLRAQYPQVEVRCGELDAE 65
H +VVVLG +G+S+V++L + L V+DTR+NPP L Q VE+ G + +
Sbjct: 8 HNVVVVGLGITGLSVVKHLRKTQPQLTVKVIDTRDNPPGAERLPEQ---VELHRGGWNTQ 64

Query: 66 FLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTT 125
+L A + +PG++L TP + AKG + GDI+LFA P+VAITGSN KSTVT
Sbjct: 65 WLAEADLVVTNPGIALATPEIQTVLAKGTPVVGDIELFAWAVNKPVVAITGSNGKSTVTD 124

Query: 126 LVGEMAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVS 185
L G MA AA V VGGN+G PAL+LL D +LYVLELSSFQLET L + A LN+S
Sbjct: 125 LTGVMAKAAGLTVGVGGNIGVPALELLEQDADLYVLELSSFQLETTSSLKLKAAAFNLNLS 184

Query: 186 EDHMDRYDGMADYHLAKHRIFRGARQVVVNRRADALTRPLIADTVPCWSFGLNKPDKAFG 245
EDHMDRY+GMADY AK RIF A VVNR D T P + +P +FG D +A+G
Sbjct: 185 EDHMDRYEGMADYRAAKLRIFDHAEALAVVNRDDQETYPEV--EMPVVTFG---SDEQAYG 239

Query: 246 LIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSG 305
L + + WL +++ ELK+ G HN +N A G+ + L ALK ++G
Sbjct: 240 LEVDGSRTWLLDHGQRVIASDELKLVGKHNLANALVLLALLKAAGVDYHNALNALKNYTG 299

Query: 306 LAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLR 365
L HRCQ V + +GV + +DSKATN+ + GKL LL GG GKGADF L+
Sbjct: 300 LTHRCQVVADNRGVKWVNDKATNI--ASTMAALSGLESTGKLYLLVGGVVGKGADFTPLK 357

Query: 366 EPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACA 425

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      A      +      G D      +A      +R      T+++ ++Q +      + GD V+LSPACA
Sbjct: 358 PIFATLNLQLCCFGLDGDGDFMPLHESA---IRFNTMEDVIQQISSQLKSGDMVMLSPACA 414

Query: 426 SLDMFKNFEERGRLFAKAVEELA 448
      S D F NF  RG  FA  ++ A
Sbjct: 415 SFDQFDNFMARGDAFAVLAQKYA 437

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tr Q7NPZ7 UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) 453
      [MURD] AA
      [Chromobacterium violaceum] align

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Score = 314 bits (805), Expect = 2e-84
 Identities = 191/443 (43%), Positives = 250/443 (56%), Gaps = 17/443 (3%)

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Query: 12  VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSAR 71
      VVGLG SG++ RYLA G V D + LA L P VEV G D A
Sbjct: 10  VVGLGSGSLAAARYLAAHGARVRVADANPSAERLAELEERCLPGVEVMVGAFDDATFAGAE 69

Query: 72  ELYVSPGLSLRTPALVQAAKGVRISGDIDLFAREAK---APIVAITGSNAKSTVTTLVG 128
      L VSPG+ L PA+ G + GDI++ AR + + ++AITGSN KSTVT+LVG
Sbjct: 70  LLVSPGPVPLANPAIAAFRRAGGEVVGDIIEILARAIQGDGSKVIAITGSNGKSTVTSLVG 129

Query: 129 EMAVAADKRVAVGGNLTGPALD-LLADDI-----ELYVLELSSFQLETCDRNLNAEVATVL 182
      + AA V GN+G L+ LLA + +++VLELSSFQLE+ L A+ ATVL
Sbjct: 130 HLCEAAGLDTVVAGNIGLAVLEALLAREQSGKRPDVVLELSSFQLESTFSLAADAATVL 189

Query: 183 NVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPDPFK 242
      N+SEDH+DRY + DY AK R+F G V+N+ DAL R ++ P F LN
Sbjct: 190 NISEDHLDRYADLLDYAHAKTRVFNGKGVQVLNKDDALVRAMVRPGHPVKWFSLNG---A 246

Query: 243 AFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKA 302
      A + +G WL +K+ +++++G HN +N +GLP + +L LK
Sbjct: 247 ADYALARNGGYWLKVDGEKVFDCADMQLQGLHNAANALALGLCQIGLPLEKLLDGLKT 306

Query: 303 FSGLAHRQCQVWRERQGVSYDDSKATNVXXXXXXXXXXXXXIDGKLVLLAGGDGKGADFH 362
      F GLAHR + V E G+++ DDSK TNV + VL+AGGDGKG DF
Sbjct: 307 FRGLAHRVELVDEFDGIADFIDDSKGTNVGATEAALNGMTRQV----VLIAGGDGKGQDFA 362

Query: 363 DLREPVARFCRAVVLLGRDAGLIAQAL-GNAVPLVRVATLDEAVRQAAELAREGDAVLLS 421
      L+ R RAV+L+GRDAG I AL + + L R TL+EA R+AA LAR GD VLLS
Sbjct: 363 PLKPACQRIARAVLLIGRDAGRIEAALEDGLALERCDTLEEATRRAAALARPGDVVLLS 422

Query: 422 PACASLDMFKNFEERGRLFAKAV 444
      PACASLDMFKN+ R ++F V
Sbjct: 423 PACASLDMFKNYAHRAQVFIDTV 445

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tr Q7MNV3 UDP-N-acetylmuramoylalanine-D-glutamate ligase [VV0612] 442
      [Vibrio AA
      vulnificus (strain YJ016)] align

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Score = 313 bits (803), Expect = 3e-84
 Identities = 181/440 (41%), Positives = 248/440 (56%), Gaps = 10/440 (2%)

Query: 11 IVVGLGKSGMSLVRYLARRG--LPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLC 68
 +VVGLG +G+S+VR+L + L V+DTR PP + L P + + G + +L
 Sbjct: 11 VVVGLGITGLSVVRHLRKTQPOLQVKVIDTRTPPGVEQLP---PDIALHVGSWNEAWLA 67

Query: 69 SARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVG 128
 A + +PG++L TP + A+GV + GDI+LFA A P++AITGSN KSTVT L G
 Sbjct: 68 EADLVVTNPGIALATPQIQTVLARGVAVVGDIELFAWAADKPVIAITGSNGKSTVTDLTG 127

Query: 129 EMAVAADKRVAVGGNLGT PALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDH 188
 MA A + A+GGN+G PALDLL ++ELYVLELSSFQLET L+ A LN+SEDH
 Sbjct: 128 VMANACGVKCAIGGNIGVPALDLLEQEVELYVLELSSFQLETTTSLHLVAAAFLNLSHEDH 187

Query: 189 MDRYDGMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKAFGLIE 248
 MDRY GM DY AK RIF+ A+ VVNR D T P + + D K FG++
 Sbjct: 188 MDRYQGMDDYRQAKLRIFQHAKHGVVNRRDRTYPETSHGQQSLALVTFGSDDKFEGVMS 247

Query: 249 EDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAH 308
 G+ WL++ +L ELK+ G HN +N G+ + L ALK+++GL H
 Sbjct: 248 HQGESWLSYNQQPILASRELKLVGQHNVANVLVLLAL LTCAGIDYRKGLSALKSYTGLTH 307

Query: 309 RCQVWRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFDHDLREPV 368
 RCQ V + +G+ + +DSKATN+ + GKL LL GGDGKGADF L+ +
 Sbjct: 308 RCQVVADNRGIKWVND SKATNL--ASTQAALSGLNCAGKLYLLVGGDGKGADFSPLKPIL 365

Query: 369 ARFCRAVVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDAVLLSPACASLD 428
 A+ + G D +A R +++ + + + GD V+LSPACAS D
 Sbjct: 366 AQLNLQLCCFGADGDQFMPLHASA---TRFERMEDVIEHISPQLQSGDMVMLSPACASFD 422

Query: 429 MFKNFEERGRFLFAKAVEELA 448
 F NF RG FA+ + A
 Sbjct: 423 QFSNFMARGDRFAELARQYA 442

tr Q7VP56 UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD] 435
 [Haemophilus
 ducreyi] AA
 align

Score = 311 bits (797), Expect = 1e-83

Identities = 191/442 (43%), Positives = 252/442 (56%), Gaps = 28/442 (6%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSAR 71
 +VGLGK+G+S V + A + V+DTRE P + L V + G L+ E+L ++
 Sbjct: 13 IVGLGKTGLSCVAFFAEKQATIQVIDTREQPAIEHLS---DNVALHTGSLNLEWLLASD 69

Query: 72 ELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEMA 131
 + +SPGL+L TP + A G+ + GDI+LF REAKAPI+AITGSN KSTVTTLV EMA
 Sbjct: 70 LIVMSPGLALATPEIQTAIQAGIEVVGDIELFVREAKAPIIAITGSNGKSTVTTLVSEMA 129

Query: 132 VAADKRVAVGGNLGT PALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDHMDR 191
 A +V +GGN+G PAL LL EL+VLELSSFQLET L A+ AT+LNVS+DHMDR
 Sbjct: 130 QQAGIKVGMGGNIGIPALSLLNKG YELFVLELSSFQLETTYSLKAKAATILNVSQDHMDR 189

Query: 192 YDGMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKAFGLIEEDG 251
 Y Y AK RI+ A V+VN D LT PL P S G + + F E D
 Sbjct: 190 YASGEHYRQAKLRIYENA EYVIVNDDDLTYPL-----PSQSVG----NLRHFA--EHDA 238

Query: 252 QKWLAQFDKL-----LPVGELKIRGAHNSNXXXXXXXXXGHAVGLPFDAMLGALKAFS 304
 Q A ++D+L + ++ + G HN N A G+ ++ L+ +
 Sbjct: 239 Q--YAIKYDQLCSGDQAVINTDQMLLTGRHNQLNALAAIALAEAAGINRTGIINGLR CYG 296

Query: 305 GLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDL 364
 GLAHR Q V GV + +DSKATNV + G L LL GGDGKGADF L
 Sbjct: 297 GLAHRFQVRPTNDGVCWVNDKATNV--GSTVAALNGLPLSGTLYLLLGGDGKGADFSML 354

Query: 365 REPVARFCRAVVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDAVLLSPAC 424
 + V + G+D +A+ N+ V V T+ +A+ Q L ++GD VLLSPAC
 Sbjct: 355 KALVNQPHIVCYCFGKDGKSLAELTTNS---VLVDTMQQAIEQIRPLVKQGDMLVLLSPAC 411

Query: 425 ASLDMFKNFEERGRLFAKAVEE 446
 ASLD F NFEERG +FA+ ++
 Sbjct: 412 ASLDQFNNFEERGDMFARLAQQ 433

sp Q9CPB0 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 434
 MURD_PASMU 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Pasteurella
 multocida]

Score = 301 bits (770), Expect = 2e-80
 Identities = 179/431 (41%), Positives = 247/431 (56%), Gaps = 13/431 (3%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSAR 71
 V+GLGK+G+S V +L + V+DTR P L P + G L+ ++L +
 Sbjct: 12 VIGLGKTGLSCVDFLAKQADVRVIDTRTQPAGAEQLAKNVP---LHTGSLNQWLLLED 68

Query: 72 ELYVSPGLSLRTPALVQAAAGKVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEMA 131
 + +SPGL+++TP + A A G+ + GDI+LF REAK PI+AITGSN KSTVT+LV M
 Sbjct: 69 LIIISPGLAVKTPEIQTALAAGIEVIGDIELFCREAKPIIAITGSNGKSTVTSILAHMV 128

Query: 132 VAADKRVAVGGNLGTPALDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHMDR 191
 AA +V +GGN+G PAL LL ++YVLELSSSFQLET L A ATVLN+SEDHM+R
 Sbjct: 129 NAAGLKVGMGGNIGIPALSLLAQAHDMYVLELSSSFQLETTYSLKATSATVLNISEDHMNR 188

Query: 192 YDGMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDKAFGLIEEDG 251
 Y + DY AK +I+ A+ V+N DALT + SFG + D + L E G
 Sbjct: 189 YVDLEDYRQAKLKIYHHAQTAVINAEDALT--AMDGLKNGVSFGEDNAD---YWLKTEKG 243

Query: 252 QKWLAQFDKLLPVGELKIRGAHNSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHRQ 311
 + +L + +++L E+K+ G HNY N A G+P +++ AL+ F+GL HR Q
 Sbjct: 244 RSYLMAKDERVLACDEMMLVGRHNYMNALAAIALAQAGIPLESIRRALREFNGLDHRFQ 303

Query: 312 WVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPVARF 371
 GV + +DSKATNV ++G L LL GGDGKGADF +L + +
 Sbjct: 304 LAHFAHGVRWVNDKATNV--GSTVAALTGLQLNGTLHLLLGGDGKGADFSELASLINQP 361

Query: 372 CRAVVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDAVLLSPACASLDMFK 431
 G+D +A + R +T++EA+ GD VLLSPACASLD F
 Sbjct: 362 NIICYCFGQDGEQLAALSPRS---QRFSTMEEAINALRPTLSAGDMVLLSPACASLDQFS 418

Query: 432 NFEERGRLFAK 442
 +FE+RG F +

Sbjct: 419 SFEQRGDEFTR 429

sp Q9KPG5 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC** 440
MURD_VIBCH **6.3.2.9)** AA
(**UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase**) align
(**D-glutamic acid adding enzyme**) [MURD] [Vibrio cholerae]

Score = 299 bits (766), Expect = 5e-80

Identities = 183/444 (41%), Positives = 249/444 (55%), Gaps = 20/444 (4%)

Query: 11 IVVGLGKSGMSLVRYLARR--GLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLC 68
+VVGLG +G+S+V YL + + V+DTRE PP L + V + + E+L
Sbjct: 11 VVVGLGITGLSVVNYLRKYHPSVTVQVIDTREAPPGQEQLSSD---VALHRSGWNLEWLL 67

Query: 69 SARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVG 128
+A + +PG++L TP + Q A G+ + GDI+LFA P++AITGSN KSTVT L G
Sbjct: 68 NADLVVTNPGIALATPEIQVLAAGIPVVGDIELFAWHVDTPVIAITGSNGKSTVTDLSG 127

Query: 129 EMAVAADKRVAVGNNLGTPLDILLADDIELYVLELSSFQLETCDRNLNAEVATVLNVSEDH 188
+A AA + AVGGN+G PALDL++ D+ELYVLELSSFQLET L + A LN+SEDH
Sbjct: 128 VLANAAGVKA AVGGNIGVPALDLISPDVELYVLELSSFQLETTSSLKLKAAAFNLNSEDH 187

Query: 189 MDRYDGMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKAFGLIE 248
MDRY GM DY AK RIF A VVN D T P A + +FG+ + F L +
Sbjct: 188 MDRYQGMEDYRQAKLRIFDHAETAVVNADDTQTFPDHAAHLQVVTFGVEQA--AQFSLAQ 245

Query: 249 EDGQKWLAFAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAH 308
G+++L + + ++ EL + G HN +N + G+ F L ALK+++GL H
Sbjct: 246 HQGREYLFARDEAVMACAELSLVGRHNVANVLTVLALLDSAGVNFRLALDALKSYTGLTH 305

Query: 309 RCQVWRERQGVSYDDSKATNVXXXXXXXXXXXXXIDGKLVLLAGGDGKGADFHDLREPV 368
RCQ V + G+ + +DSKATNV I+G+L LL GG GKGADF L +
Sbjct: 306 RCQVVADNHGIKWVNSKATNV--ASTLAALSGLKIEGQLYLLVGGVGKGADFTPLAPVL 363

Query: 369 ARFCRAVVLLGRDAGLIAQALGNVPLVRVA----TLDEAVRQAAELAREGDAVLLSPAC 424
A + G D +PL A +++ +R + GD VLLSPAC
Sbjct: 364 ATLVPVQLCCFGVDG-----HQFMPLHPSARFYDSMESIIRSIRPQLKSGDMVLLSPAC 416

Query: 425 ASLDMFKNFEEERGRLFAKAVEELA 448
AS D FKNF RG +FA+ + A
Sbjct: 417 ASFDQFKNFMARGDIFAQLARQYA 440

sp Q8XVI5 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC** 499
MURD_RALSO **6.3.2.9)** AA
(**UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase**) align
(**D-glutamic acid adding enzyme**) [MURD] [Ralstonia
solanacearum (Pseudomonas solanacearum)]

Score = 298 bits (762), Expect = 2e-79

Identities = 189/488 (38%), Positives = 264/488 (53%), Gaps = 52/488 (10%)

Query: 9 FRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLC 68
F +V+GLG+SG+++ R+ AR G V DTRE P L LRA P E G L

Sbjct: 9 FVLVLGLGESGLAMARWCARHGARARVADTREAPANLPALRAHVPDAEFIGGPFAPSLLE 68

Query: 69 SARELYVSPGLSLRTPALVQ---AAAKGVRISGDIDLFAR-----EAKAP-IVAIT 115
 + +SPGLS A+ A + V + G+I+LFAR + AP ++AIT

Sbjct: 69 GVALVAISPGLSPLDAAVAALLDGARERAVPVWGEIELFARALAGLKLQGYAPRVLAIT 128

Query: 116 GSNAKSTVTTLVGEMAVAADKRVAVGGNLGTPALDLLADDIE-----LYVLELSSSFQLE 169
 G+N K+T T L G + A K V V GN+ ALD L + ++ ++VLELSSSFQLE

Sbjct: 129 GTNGKTTTTALAGALVQRAGKTVGVAGNISPSALDKLTECVDAGTLPDVWVLELSSSFQLE 188

Query: 170 TCDRLNAEVATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTV 229
 T L+A+ AT+LN+++DH+D + MA Y AK RIF V+NR DA

Sbjct: 189 THTLADADAATILNITQDHLDDHGSMAAYAAAKGRIFGAGTVRVLNRQDADVMAFAGKRG 248

Query: 230 PCWSFGLNKPDPF-KAFGLIEEDGQKWLA-----QFDK 261
 +FG ++P +A GL+ + G W+ + +

Sbjct: 249 GDVTFGTDEPATPEALGLLRDGGIPWIVLAEADDDDLPKPARRKKGDTTPAAPVPVRLKR 308

Query: 262 LLPVGELKIRGAHNYSNXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHRQCQVVRERQGVSY 321
 L+P L+IRG HN +N A+GLP A+L L+ ++G HR + + + +

Sbjct: 309 LMPADALRIRGLHNATNAMAALALCRAIGLPASALLHGLRDYAGEPHRVELIAAFDDIEF 368

Query: 322 YDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLEPVARFCRAVVLLGRD 381
 +DDSK TNV + ++VL+AGGDGKG DF L PVA++ RAVVL+GRD

Sbjct: 369 FDDSKGTNVGATVAALSG---LSKRVVLIAGGDGKGQDFSPLAAPVAQYARAVVLLIGRD 424

Query: 382 AGLIAQALGNA-VPLVRVATLDEAVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLF 440
 A I AL ++ V LV ATL+ AV++AA A+ GDAVLLSPACAS DMF+N+E R ++F

Sbjct: 425 APRIRAALADSGVELVEAATLEAAVQEAARAQAGDAVLLSPACASFDMFRNYEHRAQVF 484

Query: 441 AKAVEELA 448
 +AV LA

Sbjct: 485 HEAVAALA 492

tr Q7VQI9 UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase (EC 6.3.2.9) 444 AA
 [MURD] [Candidatus Blochmannia floridanus]
[align](#)

Score = 280 bits (717), Expect = 3e-74

Identities = 172/439 (39%), Positives = 241/439 (54%), Gaps = 8/439 (1%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +++G GK+G+S + + RG+ ++DTR+ P E+ L + VE G L+ ++ +A

Sbjct: 11 VIIGFGKTGLSCLNFFLIRGVIPKIIDTRQYPSEMKNLPSF---VEYCFGRNLDFWILNA 67

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSSNAKSTVTTLVGEM 130
 + VSPG+ L P +++A G+ + GDI+LF RE API+AITGSN KSTVT LV +M

Sbjct: 68 NLIVVSPGVRLDHPHIIIEAMKLGIEVVGDIELFVREISAPIIAITGSNGKSTVTQLVSKM 127

Query: 131 AVAADKRVAVGGNLGTPALDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHMD 190
 A A V V GN+G P L LL ELYVLE+SSFQL+ L A AT+LN+S DHMD

Sbjct: 128 AKQAGWSVGVAGNIGVPVLSLLKKQYELVLEISSFQLDVTYSLRATAATILNISVDHMD 187

Query: 191 RY-DGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPDPFKAFGLIEE 249
 RY G+ +Y +K RI+ + VVN +D LT+PL+ D + SF +N + L

Sbjct: 188 RYPKGLEEYICSKKRIYHNSYFCVVNDSPLTKPLLNDGIYHVSFSMNSKS-ADYRLEY 246

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNSYNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
 G W+ + +L ELKI NY N V +P L L+ FSGL+HR

Sbjct: 247 KGNNWIVANGEYVLSCAELKINNCNMNMLSLALSDIVKIPRIVSLQVLRFFSGLSHR 306

Query: 310 CQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDI-DGKLVLLAGGDGKGADFHDLREPV 368
 Q V + + V + +DSKATNV + DG L LL GGDGK A+F +L +

Sbjct: 307 FQLVYKNRNVWCWINDSKATNVGATKEAINNTIITLRDGNLHLLLGGDGKLANFFELSCLI 366

Query: 369 ARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACASLD 428
 + + G+D + Q+ N V L + +A+ + + D VLLSPACASLD

Sbjct: 367 KHYAIHLYCFGKDGVCVTQSGFNDVFLSN--NIIDAMYIISRRVQRKDIVLLSPACASLD 424

Query: 429 MFKNFEERGRFLFAKAVEEL 447
 F +F RG LF + L

Sbjct: 425 QFSSFRARGNLFTYLAQRL 443

sp Q8D2Z4 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 438
 MURD_WIGBR 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Wigglesworthia
 glossinidia brevipalpis]

Score = 276 bits (707), Expect = 4e-73

Identities = 164/441 (37%), Positives = 250/441 (56%), Gaps = 17/441 (3%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRC--GELDAEFLC 68
 +++GLG +G+S V + +RG+ ++D +P L +Y ++ C G L+ ++L

Sbjct: 10 VIIGLGITGLSCVNFYKRGIKTYIMDDSYSPEYL-----KYVPYDIPCHLGSLNVKWL 64

Query: 69 SARELYVSPGLSLRTPALVQAAAGVRIISGDIDLFAREAKAPIVAITGSNAKSTVTTLVG 128
 +A+ + +SPG+SL P+L+ A + I GDI+LFAREA PI+AITGSN KSTVT+++G

Sbjct: 65 NAKLIIISPVS LYHPSLIIAKKLNIEIIGDIELFAREASRPPIAITGSNGKSTVTSMIG 124

Query: 129 EMAVAADKRVAVGGNLGTPALDLLAD-DIELYVLELSSSFQLETCDRLNAEVATVLNVSED 187
 +A+ + V +GGNLGTPALDLL + +LY++ELSSSFQLET L +++LNV+ D

Sbjct: 125 AIALNSGLSVGIGNLGTPALDLLNEKSYQLYIELSSSFQLETTFNLKTASSILNVTHD 184

Query: 188 HMDRYD-GMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDKAFGL 246
 HMDRY G+ Y L K +I++ A+ ++N D +T P+ + C F +K + +

Sbjct: 185 HMDRYPLGINQYRLIKLKIYKNAVKIINLDDYMTWPVHKNSVCIGFSSHK--GKYCI 241

Query: 247 IEEDGQKWLAQFDKLLPVGELKIRGAHNSYNXXXXXXXXXGHAVGLPFDAMLGALKAFSGL 306
 + W+ LL E+KI G HNY N + +P + L LK FSGL

Sbjct: 242 KKHKKNNWMVNNKFLKCEMKISGFHNYLNALVSLIFSDILKIPREISLNTLKNFSGL 301

Query: 307 AHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLRE 366
 HR Q + ++ +S+ +DSK+TNV I G + LL GGD K A+ L +

Sbjct: 302 PHRFQIIHKNNISWINDSKSTNV--SSTIAALSSIKIKGNIHLLLGGD SKKANLLPLMK 359

Query: 367 PVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACAS 426
 + + G+DA L+++ + TL ++ + E GD VLLSPAC+S

Sbjct: 360 IIRNKKIKLYCFGKDAYLLSKI---STDSFINDTLYHSMIKIKENLNHGDIVLLSPACSS 416

Query: 427 LDMFKNFEERGRLEFAKAVEEL 447
LD FKNF+ERG F K +++
Sbjct: 417 LDQFKNFKERGEKFTKLAQKI 437

tr Q7W4B2 Putative peptidoglycan synthesis protein [MURD] [Bordetella 508 AA
parapertussis]

align

Score = 268 bits (686), Expect = 1e-70
Identities = 185/491 (37%), Positives = 251/491 (50%), Gaps = 57/491 (11%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVR----CGE-LDAE 65
+++GLG++G++ R+ AR+G P V DTR P LA L+A V CGE +
Sbjct: 15 LILGLGETGVAAARWCARQGSPLRVADTRAQPGGLAALQAALADATVEYRLGCCEQFPDP 74

Query: 66 FLCSARELYVSPGL----SLRTPALVQAAKGVRISGDIDLFAR-----EAKAPIV 112
L ++ +SPGL S L QA + V + G+I+LFAR E + ++
Sbjct: 75 LLDGVAQIVLSPGLVPHESTRELLEQARERNVEVGEIELFARALAGLAESREYRPRVL 134

Query: 113 AITGSNAKSTVTTLVGEMAVAADKRVAVGGNLTGTPALDLLADDIE-----LYVLELSSF 166
AITG+N K+TVT L ++ A GN+ AL L D ++ ++VLELSSF
Sbjct: 135 AITGTNGKTTVTALTRQLIEAGGMSARAAGNISPAALAALIDALDQDDLQVWVLELSSF 194

Query: 167 QLETCDRLNAEVATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIA 226
QLET L + A VLN++DH+D + M Y AK RI + AR +VNR D LT ++
Sbjct: 195 QLETTRTLAPDAAVVLNVTDHLDWHGDMQAYAQAKARILKPARLAIVNRDDPLTVAMVE 254

Query: 227 D--TVPCWSFGLNKPDKFA-FGLIEEDGQKWLA-----Q 258
+ SFG + P GL G WL +
Sbjct: 255 SLQALNVRSFGRDVPALVGDMGLELGQGVAWLTACESNDFDEPAPRRKKDAPPPTRAGGR 314

Query: 259 FDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHRCQWVRERQG 318
+L+PV L+IRG HN N ++ L + ML L+ ++G HR + VR
Sbjct: 315 MSRLMPVDALRIRGVHNALNALAAMQLARSLDLGWGPMRLRTLRYAGEPHRAELVRSIGD 374

Query: 319 VSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLEPVARFCRAVVLL 378
V Y +DSK TNV + ++VL+AGG GKG DF L V R RAVVL+
Sbjct: 375 VDYINDSKGTNVGATVAALEG----LGQQVLIAGGQKGQDFSPVLPVRRHARAVVLI 430

Query: 379 GRDAGLIAQALG-NAVPLVRVATLDEAVRQAELAREGDAVLLSPACASLDMFKNFEERG 437
G D I + L VP V A + EAVR+AAELA+ GDAVLLSPACAS DMF+N+ RG
Sbjct: 431 GVDGAAIGKVLEPTGVPCVAAADMREAVRRAELAQPDAVLLSPACASFDMFRNYPHRG 490

Query: 438 RLFAKAVEELA 448
+FA V+ELA
Sbjct: 491 EVFAAEVQELA 501

tr Q7WFS0 Putative peptidoglycan synthesis protein [MURD] [Bordetella 510 AA
bronchiseptica (Alcaligenes bronchisepticus)]

align

Score = 268 bits (684), Expect = 2e-70
Identities = 185/493 (37%), Positives = 251/493 (50%), Gaps = 59/493 (11%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVR---CGE-LDAE 65
 +++GLG++G++ R+ AR+G P V DTR P LA L+A V CGE +
 Sbjct: 15 LILGLGETGVAAARWCARQGSPLRVADTRAQPGGLAALQAALADATVEYRLGCGEQFPPD 74

Query: 66 FLCSARELYVSPGL---SLRTPALVQAAAKGVRISGDIDLFAR-----EAKAPIV 112
 L ++ +SPGL S L QA + V + G+I+LFAR E + ++
 Sbjct: 75 LLDGVAQIVLSPGLVPHEPTRELLEQARERNVEVVGEIELFARALAGLAESREYRPRVL 134

Query: 113 AITGSNAKSTVTTLVGEMAVAADKRVAVGGNLTGTPALDLLADDIE-----LYVLELSSF 166
 AITG+N K+TVT L ++ A GN+ AL L D ++ ++VLELSSF
 Sbjct: 135 AITGTNGKTTVTALTRQLIEAGGMSARAAGNISPAALAALIDALDQDDLQVWVLELSSF 194

Query: 167 QLETCDRLNAEVATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVNRADALTRPLI- 225
 QLET L + A VLN++DH+D + M Y AK RI + AR +VNR D LT ++
 Sbjct: 195 QLETTRTLAPDAAVVLNVTQDHLDDHGMQAYAQAKARILKPARLAIVNRDDPLTVAMVE 254

Query: 226 -ADTVPCWSFGLNKPDFKA-FGLIEEDGQKWLA----- 257
 + SFG + P GL G WL
 Sbjct: 255 SLQALNVRSFGRDVPALVGDMGLELGGVAVWLTAESNDFDEPAPAPRRKKDAPPPTRAG 314

Query: 258 -QFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHRCQWVRER 316
 + +L+PV L+IRG HN N ++ L + ML L+ ++G HR + VR
 Sbjct: 315 GRMSRLMPVDALRIRGVHNALNALAAMQLARSLDLGWGPMLRTLRYAGEPHRAELVRSI 374

Query: 317 QGVSYDDSKATNVXXXXXXXXXXXXDIDGLVLLAGGDGKGADFDLREPVARFCRAVV 376
 V Y +DSK TNV + ++VL+AGG GKG DF L V R RAVV
 Sbjct: 375 GDVDYINDSKGTNV---GATVAALEGLGQVVLIIAGGQKGQDFSPLPVVRHARAVV 430

Query: 377 LLGRDAGLIAQAL-GNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACASLDMFKNFEE 435
 L+G D I + L VP V A + EAVR+AAELA+ GDAVLLSPACAS DMF+N+
 Sbjct: 431 LIGVDGAAIGKVLEPTGVPCVAAADMREAVRRAAELAQPGDAVLLSPACASFDMFRNYPH 490

Query: 436 RGRLFAKAVEELA 448
 RG +FA V+ELA
 Sbjct: 491 RGEVFAAEVQELA 503

sp P57313 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 440
 MURD_BUCAI 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Buchnera
 aphidicola (subsp. Acyrthosiphon pisum) (Acyrtosiphon
 pisum symbiotic bacterium)]

Score = 263 bits (671), Expect = 6e-69

Identities = 147/440 (33%), Positives = 244/440 (55%), Gaps = 14/440 (3%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQ-VEVRCGELDAEFLCS 69
 +++G+G +G+S + + ++G+ ++D ++P + PQ +E G LD +++
 Sbjct: 11 LILGMGLTGISCINFFLKKGIKPKIIDESKHPSNFIKI----PQNI EYSLGSLDHQWILE 66

Query: 70 ARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129
 + + +SPG+S P L++A G+ I DI+LF+RE PI++ITG+N KSTV T++ +
 Sbjct: 67 SDLIVISPGISSFKPILIKARLLGIEIISDIEIFSREVTCPPIISITGTNGKSTVATMIEK 126

Query: 130 MAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHM 189
+A + + +GGN+G P L++L + +LY++ELSSFQLE L +++A +LN+SEDH+
Sbjct: 127 IAKKSGYKAFLLGGNIGVPVLEILDKEADLYIELSSFQLENTFNLKSKIIVILNISEDHI 186

Query: 190 DRY-DGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCW-SFGLNKPDKFAFGLI 247
+RY +G Y K ++ A ++N D + + LI W SFG N+ D++ +
Sbjct: 187 NRYPNGFQQYKNTKLSVYNQAEICIIINSNDKIEKSLIHSKNKKWISFGTNRSDYR---IC 243

Query: 248 EEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLA 307
+ L F+ K+L E+ + G HNY+N A+ P + + LK+FS L
Sbjct: 244 SKSNDPILFFKNKKILNTSEILLYGYHNNYNNILVSLAISDAMQFPRNDAINVLKSFSLNP 303

Query: 308 HRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDREP 367
HR Q ++ +GV + +DSK+TNV G + LL GGD K A+F+ L+
Sbjct: 304 HRFQIIKNEKGVWRWINDSKSTNVNSTQVALNSIKT--TGTIRLLLGGDSKSANFNILKNI 361

Query: 368 VARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACASL 427
+ GRD +++ + V L +AV ++ + GD VLLSP C+SL
Sbjct: 362 FRTLKIKIYCFGRDGIKLSKICEK--KSIYVENLKKAVILISKQVKSQVSGDTVLLSPGCSSL 419

Query: 428 DMFKNFEERGRLFAKAVEEL 447
F NFEERG LF K ++E+
Sbjct: 420 GQFSNFEERGNLFIKLIKEI 439

tr Q7VUQ1 Putative peptidoglycan synthesis protein [MURD] [Bordetella 510 AA
pertussis]

align

Score = 262 bits (669), Expect = 1e-68
Identities = 182/493 (36%), Positives = 248/493 (49%), Gaps = 59/493 (11%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVR----CGE-LDAE 65
+++GLG++G++ R+ AR+G P V D+R P LA L+A V CGE +
Sbjct: 15 LILGLGETGVAAARWYARQGSPLRVTDRAQPGGLAALQAALADATVEYRLGCGEQFPPD 74

Query: 66 FLCSARELYVSPGL----SLRTPALVQAAKGVRISGDIDLFAR-----EAKAPIV 112
L ++ +SPGL S L QA + V + G+I+LFAR E + ++
Sbjct: 75 LLDGVAQIVLSPGLVPHPESPTRELLEQARERNVEVVGEIELFARALAGLAESREYRPRVL 134

Query: 113 AITGSNAKSTVTTLVGEMAVAADKRVAVGGNLGTPALDLLADDIE-----LYVLELSSF 166
AITG+N K+TVT L ++ A GN+ AL L D ++ ++VLELSSF
Sbjct: 135 AITGTNGKTTVTALTRQLIEAGGMSARAAGNISPAALAALMDALDQDDLQVQVWVLELSSF 194

Query: 167 QLETCDRLNAEVATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLI- 225
QLET L + A VLNV++DH+D + M Y AK RI + AR +VNR D L ++
Sbjct: 195 QLETTRTLAPDAAVVLNVTQDHLWDHGMQAYAQAKARILKPARLAIVNRDDPLAVAMVE 254

Query: 226 -ADTVPCWSFGLNKPDKFA-FGLIEEDGQKWLA- 257
+ SFG + P GL G WL
Sbjct: 255 SLQALNVRSFGRDVPALVGDMGLELGGQVAWLTADESNDFDEPAPAPRRKKDAPPPTRAG 314

Query: 258 -QFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHRCQWVRER 316
+ +L+PV L+IRG HN N ++ L + ML L+ ++G HR + VR
Sbjct: 315 GRMSRLMPVDALRIRGVHNALNALAAMQLARSLDLGWGPMRLTLRDYAGEPHRAELVRSI 374

Query: 317 QGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPVARFCRAVV 376
V Y +DSK TNV + ++VL+AGG GKG DF L V R RAVV
Sbjct: 375 GDVDYINDSKGTNV---GATVAALEGLGQQVLIAGGQKGQDFSPLVPVRRHARAVV 430

Query: 377 LLGRDAGLIAQAL-GNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACASLDMFKNFEE 435
L+G D I + L VP A + EAVR+AAELA+ GDAVLLSPACAS DMF+N+
Sbjct: 431 LIGVDGAAIGKVLEPTGVPCAAAADMREAVRRAELAQPDAVLLSPACASFDMFRNYPH 490

Query: 436 RGRLFAKAVEELA 448
RG +FA V ELA
Sbjct: 491 RGEVFAAEVRELA 503

sp Q89AQ2 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 442
MURD_BUCBP 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Buchnera
aphidicola (subsp. Baizongia pistaciae)]

Score = 252 bits (643), Expect = 1e-65
Identities = 146/440 (33%), Positives = 238/440 (53%), Gaps = 13/440 (2%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
++ G+G +G+S + + +G+ ++DT + P + + ++ + G ++ ++ +
Sbjct: 11 LIFGMGLTGISCLNFFLSKGIYPKIMDTDKRPKHIEKI-IKFKNICYHTGSVNYSWILQS 69

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+ VSPG++ PAL A K + I GDI+LF +E K PI+AITGSN KS+VT +V E+
Sbjct: 70 NLIIVSPGITPSHPALKFATKKNIEIIGDIELFVQETKVPIIAITGSNGKSSVTKIVKEI 129

Query: 131 AVAADKRVAVGGNLGTPLDLLADDIELYVLELSSSFQLETCDRLNAEVATVLNVSEDHMD 190
A +GGN+G PAL+++ ++LELSSFQLE L A +AT+LN++ DH++
Sbjct: 130 IQKAGFTTYIGGNIGIPALNIVNKFHFFILELSSSFQLERTFSLKAYIATILNITPDHLN 189

Query: 191 RYDG-MADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDKFAFLIEE 249
RY + +Y AK +I++ ++ ++N + +T A C SFG++ D+ L
Sbjct: 190 RYSSDIKEYEKAKQKIYKNSKICIINVDNPVTINRQAQLTKCISFGVHSGDYH---LSHT 246

Query: 250 DGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXGHAVGLPFDAMLGALKAFSGLAHR 309
WL ++ KL+ +LK+ G HNY N H + + F + LK F GL HR
Sbjct: 247 YTNTWLCYKSLKLINTKKLKLSGRHNYINMLSALAIVHELKISFKISVRILKNFLGLPHR 306

Query: 310 CQVVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPVA 369
CQ V + +++ +DSK+TN+ + GK+ L+ GGD K ++ + L+ +
Sbjct: 307 CQKVYKNNNITWINDSKSTNI--ASTKSAIQSINTKGKIRLILGGDKKSSNLNLLKPILK 364

Query: 370 RFCRAVVLLGRDAGLIAQALGNAVPLVR--VATLDEAVRQAAELAREGDAVLLSPACASL 427
+ G+D + L N P TL E ++ + + GD VLLSPAC+SL
Sbjct: 365 NNAIVIYCYGKD---KKELFNLYPHKSKIFETLQEVMOHISVQVQPGDVVLLSPACSSL 420

Query: 428 DMFKNFEERGRLFAKAVEEL 447
D F FEERG F K ++EL
Sbjct: 421 DQFSGFEERGNTFVKLIQEL 440

sp Q9JSZ5 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 445
MURD_NEIMA 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Neisseria
meningitidis (serogroup A)]

Score = 250 bits (639), Expect = 3e-65
Identities = 164/446 (36%), Positives = 233/446 (51%), Gaps = 18/446 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+V GLG +G+S++ YL + G A D P ++ + + + G L
Sbjct: 9 LVAGLGGTGISMIAYLKNGAEVAAYDAELKPERVSQIGKMFDDLGVFYTGRLKDALSNGF 68

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFA---REAKAPIVAITGSNAKSTVTTLV 127
L +SPG+S R P + G R+ GDI+L A ++AITGSN K+TVT+LV
Sbjct: 69 DILALSPGISERQPDIEAFKRNGGRVLGDIELLADIVNRRGDKVIAITGSNGKTTVTSLV 128

Query: 128 GEMAVAADKRVAVGGNLGTPALDLLAD---DIELYVLELSSSFQLETCDRLNAEVATVLN 183
G + + + GN+G P L+ +++VLELSSSFQLE + L ATVLN
Sbjct: 129 GYLCKICGLDTVIAGNIGAPVLEAELQREGKKADVWVLELSSSFQLENTESLRPTAATVLN 188

Query: 184 VSEDHMDRYDGMADYHLAKHRIFRGARQVVNRADALTRPLIADTVPCWSFGLNKPDFKA 243
+SEDH+DRYD + DY K +IFRG V+N DA R + F L +++A
Sbjct: 189 ISEDHLDRYDDLDDYAHTKAKIFRGDGVQVLNADDAFCRAMKRAGREVKWFSL---EYEA 245

Query: 244 -FGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKA 302
F L E G+ L + L+ ++ ++G HN +N AVGLP +A+L +K
Sbjct: 246 DFWLERETGR--LKQGNEDLIATQDIPLQGLHNATNVMAAVALCEAVGLPREALLEHVKT 303

Query: 303 FSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFH 362
F GL HR + + E+ GV + DDSK TNV + L ++ GG GKG DF
Sbjct: 304 FQGLPHRVEKIGEKNGVVFIDDSKGTNV---GATAAAIAGLQNPLFVILGGMGKGQDFT 359

Query: 363 DLREPVARFCRAVLLGRDAGLIAQAL-GNAVPLVRVATLDEAVRQAAELAREGDAVLLS 421
LR+ +A + V L+G DA I + L G + + ATL+EAV++A A GD VLLS
Sbjct: 360 PLRDALAGKAKGVFLIGVDAPQIRRDLDGCDLNMTCATLEEAVQKAYAQAEGDIVLLS 419

Query: 422 PACASLDMFKNFEERGRLFAKAVEEL 447
PACAS DMFK + R +F A + L
Sbjct: 420 PACASFDMFKGYAHRSEVFIFGAFKAL 445

sp Q8R9G4 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 450
MURD_THETN 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD]
[Thermoanaerobacter tengcongensis]

Score = 247 bits (631), Expect = 2e-64
Identities = 164/447 (36%), Positives = 246/447 (54%), Gaps = 19/447 (4%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQ--VEVRCGELDAEFLCS 69
V GLG SG++L R L G D R+N L + VE++ GE EFL
Sbjct: 10 VAGLGVSVALCRVLVNLGANVIAVD-RKNEIALKEALEELKDLPVEIKLGEFKKEEFLKG 68

Query: 70 ARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129
+ +SPG+SL + + +A G+ I G+++L R +KAPI AITG+N K+T T+L+GE

Sbjct: 69 IELVVLSPGISLESEIVKKAKDMGLEILGEVELAYRLSKAPIYAITGTNGKTTTTTSLIGE 128

Query: 130 MAAVADKRVAVGGNLGTPAL--DLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSED 187
M A ++V V GN+G P + L A + V E+SSFQLET +++ ++N++ D

Sbjct: 129 MFRNAGRKVYVAGNIGYPLIYAALAEAGPNDHIVAEISSFQLETVKEFRPKISCIINITPD 188

Query: 188 HMDRYDGMADYHLAKHRIFRGARQ--VVVNRADALTRPLIADTVPCWSFGLNKPDKAF 244
H+DR+ +Y K RIF R+ VV+N D +T L + F ++

Sbjct: 189 HLDHRKTFENYANIKGRIFENQREEEYVVLNYDDPVTWGL-KERAKAKVFPFSRKKVLEN 247

Query: 245 GLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXGHAVGLPFDAMLGALKAFS 304
G ++G +L Q K++ V ++ I G HN N + G+ DA+ L+ F

Sbjct: 248 GAYVKEG--FLYLQNKVKIKVEDIYIPGEHNLENALAASSVAYLSGIEVDAIETTLRTFK 305

Query: 305 GLAHRQCWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGLVLLAGGDGKGADFHDL 364
G+ HR ++V E +G+ +Y+DSK TN I VL+AGG KG++F +

Sbjct: 306 GVEHRIEFVAEIEGIKFYND SKGTNPDA SIKAIQALKTP I----VLIAGGYDKGSEFDEF 361

Query: 365 REPVARFCRAVVLLGRDAGLIAQ-ALGNAV P--LVRVATLDEAVRQAELAREGDAVLL 420
+ + R ++L+G+ A I + AL + P + V +L+EAVR+A E+A +GD+VLL

Sbjct: 362 VKTFDKKVRKLILIGQTAQKIKKTALKYSYPEEDIFLVSLEEAVRKAYEVAEKGDSVLL 421

Query: 421 SPACASLDMFKNFEERGRLFAKAVEEL 447
SPACAS DMFKNFEERG+ F KAV +L

Sbjct: 422 SPACASWDMFKNFEERGKAFKKAVMDL 448

sp Q9K0Y4 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 445**
MURD_NEIMB **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Neisseria
meningitidis (serogroup B)]

Score = 246 bits (627), Expect = 7e-64

Identities = 163/447 (36%), Positives = 230/447 (50%), Gaps = 20/447 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+V GLG +G+S++ YL + G A D P ++ + + + G L

Sbjct: 9 LVAGLGGTGISMIAYLKNGAEVAAYDAELKPERV SQIGKMF DGLVFYTGRLKDALDNGF 68

Query: 71 RELYVSPGLSLRTPALVQAAAGVVRISGDIDLFA-----REAKAPIVAITGSNAKSTVTT 125
L +SPG+S R P + G R+ GDI+L A R+ K ++AITGSN K+TVT+

Sbjct: 69 DILALSPGISERQPDIEAFKQNGGRVLGDIELLADIVNRRDDK--VIAITGSNGKTTVTS 126

Query: 126 LVGEMAAVADKRVAVGGNLGTPALDLL---ADDIELYVLELSSFQLETCDRLNAEVATV 181
LVG + + + GN+GTP L+ +++VLELSSFQLE + L ATV

Sbjct: 127 LVGYLCIKCLDTVIAGNIGTPVLEAEWQREGKKADVWVLELSSFQLENTESLRPTAATV 186

Query: 182 LNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPDKAF 241
LN+SEDH+DRYD + DY K +IFRG V+N DA R + F L

Sbjct: 187 LNISEHDLDYDDLDDYAHTKAKIFRGDGVQVLNADDAFCRAMKRAGREVKWFSLEHE-- 244

Query: 242 KAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXGHAVGLPFDAMLGALK 301
F L E G+ L + L+ ++ ++G HN +N A+GL +A+L +K

Sbjct: 245 ADFWLERETGR--LKQGNEDLIVTQDIPLQGLHNAANVMAAVALCEAIGLSREALLEHVK 302

Query: 302 AFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADF 361
 F GL HR + + E+ GV + DDSK TNV + L ++ GG GKG DF
 Sbjct: 303 TFQGLPHRVEKIGEKNGVVFIDDSKGTNV---GATAAAIAGLQNPLFVILGGMGKGQDF 358

Query: 362 HDLREPVARFCRAVVLLGRDAGLIAQAL-GNAVPLVRVATLDEAVRQAAELAREGDAVLL 420
 LR+ + + V L+G DA I + L G + + ATL EAV+ A A GD VLL
 Sbjct: 359 TPLRDALVGKAKGVFLIGVDAPQIRRDLDGCGLNMTDCATLGEAVQTAYAQAEGDIVLL 418

Query: 421 SPACASLDMFKNFEERGRLFAKAVEEL 447
 SPACAS DMFK + R +F +A + L
 Sbjct: 419 SPACASFDMFKGYAHRSEVFIEAFKAL 445

sp Q8K9T2 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 440
 MURD_BUCAP 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Buchnera
 aphidicola (subsp. Schizaphis graminum)]

Score = 242 bits (617), Expect = 1e-62
 Identities = 150/440 (34%), Positives = 234/440 (53%), Gaps = 14/440 (3%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +++GLG +G+S + + ++G+ V+D P L + +E + G L ++ +
 Sbjct: 11 LILGLGLTGISCINFFLKKGIQPRVIDESNKPIFLNKIPKN---IEYKLGNLKENWILES 67

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
 + +SPG+S P L++A + G+ I DI+LF+RE K PI++ITG+N KSTV T+V ++
 Sbjct: 68 DLIIISPGISFVKPILMKARSLGIDIISDIELFSRETKCPIISITGTNGKSTVATMVKKI 127

Query: 131 AVAADKRVAVGGNLGTALDLDLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDHMD 190
 A + +V +GGN+G P L++L LYVLELSSFQLET L +++A VLN++EDH+D
 Sbjct: 128 AEKSGYKVLGGNIGFPVLEMLNKKASLYVLELSSFQLETTFNLKSKIAVVLNITEDHLD 187

Query: 191 RY-DGMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFG-LNKPDKAFGLIE 248
 RY +G Y K I+ A+ ++ +P + SFG N D+ I
 Sbjct: 188 RYPEGFQYKKTLSIYNKAKICLIKKKGEKKPFNTKSKKYISFGTCNNNDY----YIN 243

Query: 249 EDGQKWLAQFD-KLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLA 307
 + +K + F + K++ + + G HNY N + + LK F GL
 Sbjct: 244 YEKEKAILFHKNKKIVDTSNILLNGHHNYENILTSLAISDQMKFDQKVSINVLLKKFLGLP 303

Query: 308 HRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDREP 367
 HR Q V +S+ +DSK+TNV I G + LL GGDGK ++F+ L++
 Sbjct: 304 HRFQTVHINNINISWINDSKSTNV--DSTKAALKNLKIKGTIWLLLGGDGKSSNFNILKKY 361

Query: 368 VARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACASL 427
 + + G+D GL L + TL +A+ ++ + GD VLLSP C+S
 Sbjct: 362 FEKIKIKIYCFGKD-GLNLSKLCKK-KSIYTKTLKQAIILISKKIQPGDVVLLSPGCSSK 419

Query: 428 DMFKNFEERGRLFAKAVEEL 447
 D F NFEERG LF K +E+
 Sbjct: 420 DQFSNFEERGNLFIKLSKEI 439

trnew AAR36463 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 452**
6.3.2.9) [MURD] **AA**
[Geobacter sulfurreducens] **align**

Score = 234 bits (598), Expect = 2e-60
Identities = 155/448 (34%), Positives = 226/448 (49%), Gaps = 19/448 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDRENPPPELATLR--AQYPQVEVRCGELDAEFLC 68
+VVGL ++G+++ R+LA +G V D R+ L A +P V G D
Sbjct: 9 LVVGLARTGVAVARFLAAQGARVTVTDLRDEAALAGPLEQLAGHP-VSYVLGRHDEADFA 67

Query: 69 SARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVG 128
+A + VSPG+ +P L A G + +I+L +R AP+VAITG+N K+T TTL G
Sbjct: 68 AAETVVVSPGVPQESPYLQAARRAGREVITEIELASRFITAPLVAITGTNGKTTTTLTG 127

Query: 129 EMAVAADKRVAVGGNLTGPALDLLADD--IELYVLELSSFQLETCDRLNAEVATVLNVSE 186
E+ R VGGN+G P ++L+ ++ V+E+SSFQLE VA +LN++E
Sbjct: 128 ELFAGCGFRTFVGGNIGNPLIELVETGAAVDRVVEISSFQLEWIRSFRPTVAVLLNITE 187

Query: 187 DHMDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADTVPCWSFGLNKPDKFA 243
DH+DRY +Y AK RIF+ V+N D + L T F +++
Sbjct: 188 DHLDRYATYQEYIDAKARIFKNQTASDWAVLNVDPIVAGLAGRTCAA-VFPMSRQRELG 246

Query: 244 FGLIEEDGQKWLAFFQF---DKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
G+ DG + F+ + P +I G HN N +G D L +
Sbjct: 247 EGIFYRDGA--IIFRHAGRQERFPTDRFRITGVHNINIMASLAAALLLGCDADRALACV 304

Query: 301 KAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
+AF GL HR + VRE GV Y++DSKATNV + L+AGG KG
Sbjct: 305 EAFGGLPHRMELVRELNGVRYFEDSKATNVGSVEKALASF-----NDITLIAGGKDKGGS 359

Query: 361 FHDLREPVARFCRAVLLGRDAGLIAQALGNVPLVRVATLDEAVRQAAELAREGDAVLL 420
+ L VA R ++L+G +A+ LG+ TL++AV AA L + G VL
Sbjct: 360 YAPLAGLVAERVHRMILIGEAKDRMARELGHLTDTRMAVTLEDAVELAASLTQPGGVVLF 419

Query: 421 SPACASLDMFKNFEERGRLFAKAVEELA 448
SPAC+S DMF+++EER + F AV+ L+
Sbjct: 420 SPACSSFDMFRDYEERAQRFRAAVDALS 447

tr Q82AD8 **Putative UDP-N-acetylmuramoylalanine-D-glutamate ligase [MURD] 467 AA**
[Streptomyces avermitilis] **align**

Score = 214 bits (544), Expect = 3e-54
Identities = 167/468 (35%), Positives = 220/468 (46%), Gaps = 45/468 (9%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVV---DTRENPPPELATLRAQYPQVEVRCGELDAEFLC 68
V GLG SG+ R L G VV D + + A L A + VR G D L
Sbjct: 11 VAGLVSGIPAARVLHGLGAVTVVNDGDDERSRAQAADLEAL--GITVRLG--DGATLP 66

Query: 69 SARELYVS-PGLSLRTPALVQAAAKGVRISGDIDLFAF---EAKAPIVAITGSNAKSTVT 124
EL V+ PG P AA GV + GD++L R AP +A+TG+N K+T
Sbjct: 67 EGTELIVTTTPGWQPKPLFAAAAEAGVPVWGDVELAWRLRGPSPAPWLAVTGTNGKTTTV 126

Query: 125 TLVGEMAVAADKRVAVGGNLTGPALDLLADD--IELYVLELSSFQLETCDRLNAEVATVL 182
++ + AA R A GN+G LD + + ++ +ELSS+QL L A ATVL

Sbjct: 127 QMLASILTAAGLRRTAAVGNIGVSLDDAVLGEETYDVLLEVELSSYQLHWAPSLRAHSATVL 186

Query: 183 NVSEDHMDRYDGMADYHLAKHRIFRGARQVVV-NRADALTRPLIA-----DTVPCWSFGL 236
 N++ DH+D + M Y K RI+ G R V N AD T L+ + F L

Sbjct: 187 NIAPDHLDDHWSMEAYTADKGRIYEGNRVACVYNVADKATEDLVRAADVEEGCRAVGFTL 246

Query: 237 NKPDFKAFGLIE-----EDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGH 287
 P G++E ED QK +L V ++ HN +N

Sbjct: 247 GTPGPSQLGVVEGILVDRAFVEDRQK---NAQELAEVADVHPPAPHNIANALAAAALAR 302

Query: 288 AVGLPFDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGK 347
 A G+P A+ L+AF AHR V + GV+Y DDSKATN G

Sbjct: 303 AFGVPASAVRDGLRAFRPDARIAHVADVDGVTYIDDSKATNTHAAEASLAAY-----GS 357

Query: 348 LVLLAGGDGKGADFDHDLREPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDE---- 403
 +V +AGG KGA F +L A+ R VVL+G D LI +AL P V V LD

Sbjct: 358 IVWIAAGGLAKGASFDLVAKSAQRLRGVVLIGADRALIREALARHAPEVPVVDLDRDTG 417

Query: 404 ----AVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLEFAKAVEEL 447
 AV++A LA GD VLL+PACAS+DMF N+ +RG FA+AV L

Sbjct: 418 AMPAAVQEARRLAVAGDTVLLAPACASMDMFANYNKRGDFAFAEAVRGL 465

trnew AAS42861 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 450**
6.3.2.9) [MURD] **AA**
[Bacillus cereus ATCC 10987] **align**

Score = 207 bits (528), Expect = 2e-52

Identities = 153/448 (34%), Positives = 223/448 (49%), Gaps = 22/448 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V+G+ KSG + L + G V D + + Q ++V CG E L

Sbjct: 13 LVLGIAKSGYAAATLLQKLGANVIVNDGKPLAENVLAELQAKGMDVVCGGHPLELLERN 72

Query: 71 RELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129
 L V +PG+ P LV A K + I +++L R ++AP V ITGSN K+T T L E

Sbjct: 73 ISLVVKNPGIPYSNPILVAAKEKQIPIVTEVELAYRISEAPFVGITGSNGKTTTMTLTFE 132

Query: 130 MAVAADKRVAVGGNLGTPALDLLAD--DIELYVLELSSFQLETCDRLNAEVATVLNVSED 187
 M K + GN+GT A ++ D + E+ V ELSSFQL + ++A LN+ E

Sbjct: 133 MLKEGQKHPVIAGNIGTVACEVAQDAKENEVVTELSSFQLMGVELFQPKIAAFLNLFEA 192

Query: 188 HMDRYDGMADYHLAKHRIFRGARQ--VVVNRADALTRPLIADTVPCWSFGLNKPDKAF 244
 H+D + +Y LAK IF+ + V+N DA L A +S G K F

Sbjct: 193 HLDYHGTTKEYGLAKANIFKNXTENDYSVINADDADVMALSA-----YSKG-QKVLFFSTT 246

Query: 245 GLIEEDG--QKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALK 301
 IE+ L F+ +K++ VG++ + G HN N +G+ +A+ LK

Sbjct: 247 KEIEDGACIKDNALYFKGEKVVEVGDIVLPGQHNLNLAAMSIAKLLGSNEAITAVLK 306

Query: 302 AFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADF 361
 F+G+ HR ++V +Y+DSKATN+ VLLAGG +G +F

Sbjct: 307 RFTGVKHRLEYVTTINNRKFYNDKATNMLATEKALSAFTQ----PTVLLAGGLDRGNEF 362

Query: 362 HDLREPVARFCRAVLLGRDAGLIAQALGNA--VPLVRVATLDEAVRQAAELAREGDAVL 419
 DL P + +A+V G+ A + +A A + V TLDEAV +A + +GD +L

Sbjct: 363 DDL-IPYFKNVKAIVTFGQTAPKLVRAAEKAGLDTIESVDTLDEAVVKAYAHSTDGDVIL 421

Query: 420 LSPACASLDMFKNFEERGRLFAKAVEEL 447

LSPACAS D FK FEERG +F +AV +L

Sbjct: 422 LSPACASWDQFKTFEERGDIFIQAVHKL 449

sp Q97RU8 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 450
MURD_STRPN 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Streptococcus
pneumoniae]

Score = 207 bits (527), Expect = 3e-52

Identities = 152/448 (33%), Positives = 228/448 (49%), Gaps = 23/448 (5%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70

+V+GL KSG S R L + G V D + A ++V G E L

Sbjct: 13 LVLGLAKSGESAARLLDKLGAIVTVNDGKPFEDNPAAQSLLEEGIKVITGGHPLELLDEE 72

Query: 71 RELYV-SPGLSLRTPALVQAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129

L V +PG+ P + +A AKG+ + +++L ++API+ ITGSN K+T TT++GE

Sbjct: 73 FALMVKNPGIPYNNPMIEKALAKGIPVLTEVELAYLISEAPIIGITGSNGKTTTTTMI 132

Query: 130 MAVAADKRVAVGGNLGTPALDL--LADDIELYVLELSSFQLETCDRLNAEVATVLNVSED 187

+ AA + + GN+G PA + +A D + V+ELSSFQL + E+A + N+

Sbjct: 133 VLTAAGQHGLLSGNIGYPASQVAQIASDKDTLVMELSSFQLMGVQEFHPEIAVITNLMPT 192

Query: 188 HMDRYDGMADYHLAKHRI---FRGARQVVVNRADALTRPLIADT---VPCWSFGLNKP 240

H+D + ++Y AK I A +V+N L + L + T VP + L K D

Sbjct: 193 HIDYHGSFSEYVAAKWNIQNKMTAADFLVLNFNQDLAKDLTSKTEATVVPFST--LEKVD 250

Query: 241 FKAFLIEEDGQKWLAFQFDKLLPVGELKIRGAHNSNXXXXXXXXXGHAVGLPFDAMLGAL 300

G EDGQ L F+ + ++ E+ + G+HN N + + L

Sbjct: 251 ---GAYLEDGQ--LYFRGEVMAANEIGVPGSHNVENALATIAVAKLRDVDNQTIKETL 304

Query: 301 KAFSGLAHRQCQVWRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360

AF G+ HR Q+V + +GV +Y+DSK+TN+ + K+VL+AGG +G +

Sbjct: 305 SAFGGVKHRLQFVDDIKGVKFYNDKSTNILATQKALSGFD---NSKVLIAGGLDRGNE 361

Query: 361 FHDLREPVARFCRAVVLLGRDAGLIAQALGNA-VPLVRVATLDEAVRQAAELAREGDAVL 419

F +L P + +V+LG+ A + +A A V V + +A R+A ELA +GD VL

Sbjct: 362 FDEL-VPDITGLKKMVILGQSAERVKRAADKAGVAYVEATDIADATRKAYELATQGDVVL 420

Query: 420 LSPACASLDMFKNFEERGRLFAKAVEEL 447

LSPA AS DM+ NFE RG LF V EL

Sbjct: 421 LSPANASWDMYANFEVRGDLFIDTVAEL 448

sp Q9S2W9 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 471
MURD_STRCO 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Streptomyces
coelicolor]

Score = 207 bits (527), Expect = 3e-52

Identities = 166/469 (35%), Positives = 220/469 (46%), Gaps = 44/469 (9%)

```
Query: 12  VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQ-VEVRCGELDAEFLCSA 70
           V GLG SG+   + L   G   VV+  ++                P   V VR G   D + L
Sbjct: 12  VAGLGVSGVPAAKVLHGLGAQVTVVNDGDDERARTQAAELEPLGVTVRLG--DGDTLPEG 69

Query: 71  RELYVS-PGLSLRTPALVQAAAKGVRISGDIDLFA-----EAKAPIVAITGSNAKSTV 123
           EL V+ PG      P   A   GV + GD++L   R           AP +A+TG+N K+T
Sbjct: 70  TELIVTAPGWKPTKPLFTAAGQAGVPVWGDVELAWRLRGLNGRKPPAPWLAVTGTNGKTTT 129

Query: 124  TTLVGEMAVAADKRVAVGGNLGTPALDLLADDIELYVL--ELSSFQLETCDRLNAEVATV 181
           ++ + AA R A GN+G   LD + + E VL   ELSS+QL      L A A V
Sbjct: 130  VQMLASILKAAGLRATAAVGNIGVSLLDAVTGEQEYDVLAVELSSYQLHWAPSLRAHSAAV 189

Query: 182  LNVSEDHMDRYDGMADYHLAKHRIFRGARQVVV-NRADALTRPLI--ADTVP-CWSFG-- 235
           LN++ DH+D + M Y   K RI+ G   V N AD T L+ AD   C + G
Sbjct: 190  LNLAPDHLDDWHGSMEAYAADKGRIYEGNHVACVYNVADKATEDLVRAADVEEGCRAIGFT 249

Query: 236  LNKPDFKAFGLIE-----EDGQKWLAFFQDKLLPVGELKIRGAHNYSNXXXXXXXXXG 286
           L P      G++E           ED QK           +L V ++      HN +N
Sbjct: 250  LGTPGPSQLGVVEGLLVDRAFVEDRQK----NAQELAEVSDVNPPAPHNIANALAAAGLA 305

Query: 287  HAVGLPFDAMLGALKAFSGLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDG 346
           A G+   A+   L+AF+  AHR   V +   GV+Y DDSKATN
Sbjct: 306  RAFGVSAAAVRDGLRAFTPDARIAHVADVDGVAYVDDSKATNTHATEASLAAYES---- 361

Query: 347  KLVLLAGGDGKGADFHDLEPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLD---- 402
           +V +AGG KGA F +L   A+ R   VL+G D LI +AL   P V V LD
Sbjct: 362  -IVWIAGGLAKGATFDELVAGAAKRLRGAVLIGADRALIREALARHAPEVPVVDLDRD 420

Query: 403  ----EAVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLEFAKAVEEL 447
           +AV++A LAR GD VLL+PACAS+DMF N+ +RG FA+AV EL
Sbjct: 421  GAMLQAVQEARRLARPGDTVLLAPACASMDMFTNYNQRGDFAQAVREL 469
```

tr Q819Q2 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)** 450 AA
[BC3912] [Bacillus cereus (strain ATCC 14579 / DSM 31)]
align

Score = 206 bits (524), Expect = 6e-52

Identities = 154/448 (34%), Positives = 225/448 (49%), Gaps = 22/448 (4%)

```
Query: 11  IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
           +V+G+ KSG +   L + G   V D +   +   Q   ++V CG   E L
Sbjct: 13  LVLGIAKSGYAAATLLQKLGANVIVNDGKPLAENVLAAELQAKGMDVVCGGHPELLELERN 72

Query: 71  RELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129
           L V +PG+   P LV A K + I   +++L R ++AP V ITGSN K+T T L E
Sbjct: 73  ISLVVKNPGIPYSNPILVAAKEKQIPIVTEVELAYRISEAPFVGITGSNGKTTTTMLTFE 132

Query: 130  MAVAADKRVAVGGNLGTPALDLLAD--DIELYVLELSSFQLETCDRLNAEVATVNLVSED 187
           M   K   + GN+GT A ++ D + E+ V ELSSFQL   +   ++A LN+ E
Sbjct: 133  MLKEGQKHPVIAGNIGTVACEVAQDAKENEVVVTELSSFQLMGVELFQPKIAAFLNLFEA 192

Query: 188  HMDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADTVPCWSFGLNKPDFKAF 244
```


H+D + +Y LAK IF+ + V+N DA L A +S G K F
Sbjct: 193 HLDYHGTTKEYGLAKANIFKNQNTENDYSVINADDADVMALSA-----YSKG-QKILFSTT 246
Query: 245 GLIEEDG---QKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALK 301
IE+ L F+ +K++ V ++ + G HN N +G +A+ LK
Sbjct: 247 KEIEDGACIKDNALYFKGEKVIEVSDIVLPGQHNLLENILAAMSIKLLGTSNEAITVVLK 306
Query: 302 AFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADF 361
F+G+ HR ++V +Y+DSKATN+ I VLLAGG +G +F
Sbjct: 307 RFTGVKHRLEYVTTINNRKFYNDKATNMLATEKALSAFTQPI---VLLAGGLDRGNEF 362
Query: 362 HDLREPVARFCRAVVLLGRDAGLIAQALGNA-VPLVR-VATLDEAVRQAAELAREGDAVL 419
DL P + +A+V G+ A + +A A + ++ V TLDEAV +A +++GD VL
Sbjct: 363 DDLI-PYFKNVKAIVTFGQTAPKLVRAAEKAGLDIIESVDTLDEAVVKAYAHSKDGDVVL 421
Query: 420 LSPACASLDMFKNFEERGRLFAKAVEEL 447
LSPACAS D FK FEERG +F +AV +L
Sbjct: 422 LSPACASWDQFKTFEERGDIFIQAVHKL 449

tr Q9ZHB0 D-glutamic acid adding enzyme MurD [MURD] 450 AA
[Streptococcus align
pneumoniae]

Score = 206 bits (523), Expect = 8e-52

Identities = 155/451 (34%), Positives = 230/451 (50%), Gaps = 29/451 (6%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVDTR---ENPPELATLRAQYPQVEVRCGELDAEFL 67
+V+GL KSG S R L + G V D + +NP L ++V G E L
Sbjct: 13 LVLGLAKSGESAARLLDKLGAIVTVNDGKPFEDNPAAQCLLEEG---IKVITGGHPLELL 69
Query: 68 CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
L V +PG+ P + +A AKG+ + +++L ++API+ ITGSN K+T TT+
Sbjct: 70 DEEFALMVKNPGIPYSNPMIEKALAKGIPVLTEVELAYLISEAPIIGITGSNGKTTTTTM 129
Query: 127 VGEMAVAADKRVAVGNGLTPALDL--LADDIELYVLELSSFQLETCDRLNAEVATVLNV 184
+GE+ AA + + GN+G PA + +A D V+ELSSFQL + E+A + N+
Sbjct: 130 IGEVLTAAGQHGLLSGNIGYPASQVAQIATDKNTLVMELSSFQLMGVQEFHPEIAVITNL 189
Query: 185 SEDHMDRYDGMADYHLAKHRI---FRGARQVVVNRADALTRPLIADT---VPCWSFGLN 237
H+D + +Y AK I A +V+N L + L + T VP + L
Sbjct: 190 MPHTIDYHGLFEEYVAAKWNINQKMTAADFLVLNFNQDLVKDLASKTEATVVPFST--LE 247
Query: 238 KPDPKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAML 297
K D G EDGQ L F+ + ++ E+ + G+HN N G+ +
Sbjct: 248 KVD----GAYLEDGQ--LYFRGEVMAANEIGVPGSHNVENALATIATAKLRGVDNQTIK 301
Query: 298 GALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGK 357
L AF G+ HR Q+V + +GV +Y+DSK+TN+ + K+VL+AGG +
Sbjct: 302 ETLSAFGGVKHRLQFVDDIKGVKFYNDKSTNILATQKALSGFD--NSKVLIAGGLDR 358
Query: 358 GADFHDLREPVARFCRAVVLLGRDAGLIAQALGNA-VPLVRVATLDEAVRQAAELAREGD 416
G +F +L P + +V+LG+ A + +A A V V + +A R+A ELA +GD
Sbjct: 359 GNEFDEL-VPDITGLKKMVILGQSAERVKRAADKAGVAYVEATDIADATRKAYELATQGD 417
Query: 417 AVLLSPACASLDMFKNFEERGRLFAKAVEEL 447

VLLSPA AS DM+ NFE RG LF V EL
 Sbjct: 418 VVLLSPANASWDMYANFEVRGDLFIDTVAEL 448

tr Q81WC9 **UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]** 450
[Bacillus AA
anthracis (strain Ames)] align

Score = 205 bits (521), Expect = 1e-51
 Identities = 152/448 (33%), Positives = 222/448 (48%), Gaps = 22/448 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V+G+ KSG + L + G V D + + Q ++V CG E L
 Sbjct: 13 LVLGIAKSGYAAATLLQKLGANVIVNDGKPLAENVLAELQAKGMDVVCGGHPLELLERN 72

Query: 71 RELYV-SPGLSLRTPALVQAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129
 L V +PG+ P LV A K + I +++L R ++AP V ITGSN K+T T L E
 Sbjct: 73 ISLVVKNPGIPYSNPILVAAKEKQIPIVTEVELAYRISEAPFVGITGSNGKTTTTMLTFE 132

Query: 130 MAVAADKRVAVGGNLGTPALDLLAD--DIELYVLELSSFQLETCDRLNAEVATVLNVSED 187
 M K + GN+GT A ++ D + E+ V ELSSFQL + ++A LN+ E
 Sbjct: 133 MLKEGQKHPVIAGNIGTVACEVAQDAKENEVVVTELSSFQLMGVELFQPKIAAFLNLFEA 192

Query: 188 HMDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADTVPCWSFGLNKPDKAF 244
 H+D + +Y LAK IF+ + V+N DA L A +S G K F
 Sbjct: 193 HLDYHGTTKEYGLAKANIFKNQTENDYSVINADDADVMALSA-----YSKG-QKVLFTST 246

Query: 245 GLIEEDG---QKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALK 301
 IE+ L F+ +K++ V ++ + G HN N +G+ +A+ LK
 Sbjct: 247 KEIEDGACIKDNALYFKAKEKVVEVDIVLPGQHNLENILAAMSIAKLLGVSNEAITAVLK 306

Query: 302 AFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADF 361
 F+G+ HR ++V +Y+DSKATN+ VLLAGG +G +F
 Sbjct: 307 RFTGVKHRLEYVTTINNRKFYNDKATNMLATEKALSAFTQ---PTVLLAGGLDRGNEF 362

Query: 362 HDLREPVARFCRAVVLLGRDAGLIAQALGNA--VPLVRVATLDEAVRQAAELAREGDAVL 419
 DL P + +A+V G+ A + +A A + V TLDEAV +A + +GD +L
 Sbjct: 363 DDL-IPYFKNVKAIVTFGQTAPKLVRAAEKAGLDTIESVDTLDEAVVKAYAHSTGDGVIL 421

Query: 420 LSPACASLDMFKNFEERGRLFAKAVEEL 447
 LSPACAS D FK FEERG +F +AV +L
 Sbjct: 422 LSPACASWDQFKTFEERGDIFIQAVHKL 449

sp Q8DQM2 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC** 450
 MURD_STRR6 **6.3.2.9)** AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Streptococcus
pneumoniae (strain ATCC BAA-255 / R6)]

Score = 204 bits (519), Expect = 2e-51
 Identities = 151/448 (33%), Positives = 227/448 (49%), Gaps = 23/448 (5%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V+GL KSG S R L + G V D + A ++V G E L

Sbjct: 13 LVLGLAKSGESAARLLDKLGAIVTVNDGKPFEDNPAAQSLLEEGIKVITGGHPLELLDEE 72

Query: 71 RELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129
 L V +PG+ P + +A AK + + ++L ++API+ ITGSN K+T TT++GE

Sbjct: 73 FALMVKNPGIPYNNPMIEKALAKRIPVLTEVELAYLISEAPIIGITGSNGKTTTTTMMIGE 132

Query: 130 MAVAADKRVAVGGNLGTPALDL--LADDIELYVLELSSFQLETCDRNLNAEVATVLNVSED 187
 + AA + + GN+G PA + +A D + V+ELSSFQL + E+A + N+

Sbjct: 133 VLTAAGQHGLLSGNIGYPASQVAQIASDKDTLVMELSSFQLMGVQEFHPEIAVITNLMPT 192

Query: 188 HMDRYDGMADYHLAKHRI---FRGARQVVVNRADALTRPLIADT---VPCWSFGLNKPD 240
 H+D + ++Y AK I A +V+N L + L + T VP + L K D

Sbjct: 193 HIDYHGSFSEYVAAKWNINQNKMTAADFLVLNFNQDLAKDLTSKTEATVVPFST--LEKVD 250

Query: 241 FKAFLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
 G EDGQ L F+ + ++ E+ + G+HN N + + L

Sbjct: 251 ---GAYLEDGQ--LYFRGEVMAANEIGVPGSHNVENALATIAVAKLRDVDNQTIKETL 304

Query: 301 KAFSGLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGLVLLAGGDGKGAD 360
 AF G+ HR Q+V + +GV +Y+DSK+TN+ + K+VL+AGG +G +

Sbjct: 305 SAFGGVKHRLQFVDDIKGVKFYNDKSTNILATQKALSGFD---NSKVVLIAAGGLDRGNE 361

Query: 361 FHDIREPVARFCRAVLLGRDAGLIAQALGNA-VPLVRVATLDEAVRQAAELAREGDAVL 419
 F +L P + +V+LG+ A + +A A V V + +A R+A ELA +GD VL

Sbjct: 362 FDEL-VPDITGLKKMVILGQSAERVKRAADKAGVAYVEATDIADATRKAYELATQGDVVL 420

Query: 420 LSPACASLDMFKNFEERGRLFAKAVEEL 447
 LSPA AS DM+ NFE RG LF V EL

Sbjct: 421 LSPANASWDMYANFEVRGDLFIDTVAEL 448

sp Q03522 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 451**
 MURD_BACSU **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) **align**
(D-glutamic acid adding enzyme) [MURD] [Bacillus
subtilis]

Score = 202 bits (513), Expect = 1e-50

Identities = 147/458 (32%), Positives = 228/458 (49%), Gaps = 28/458 (6%)

Query: 4 IASDHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELD 63
 + HF +++GL KSG + L +G+ AV D + + +EV CGE

Sbjct: 7 LQKQHF-LILGLAKSGYAAASILHEKGIYVAVNDQKPFEENEPAQKLSEKGIEVVCGEHP 65

Query: 64 AEFLCSARE--LYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKS 121
 + L +PG+ + +A +G+ + +I+L A + ITGSN K+

Sbjct: 66 VSLFDQHQITILIKNPGIPYENIMVQEAKEKGIPVWTEIELAYYLTSAKFIGITGSNGKT 125

Query: 122 TVTTLVGEMAVAADKRVAVGGNLGTPALDLL--ADDIELYVLELSSFQLETCDRNLNAEVA 179
 T TTL+ EM A ++ + GN+GT A ++ AD E V ELSSFQL E++

Sbjct: 126 TTTTLIYEMLKADSQKALIAGNIGTVASEVAYHADGDEWIVTELSSFQLMGTHAFRPEIS 185

Query: 180 TVLNVSEDHMDRYDGMADYHLAKHRIF---RGARQVVVNRADALTRPLI---ADTVPCW 232
 +LNV + H+D + +Y AK +++ + + +VN+ D L A+ VP

Sbjct: 186 LILNVFDAHLDYHHTRENYEKAKQKVYLHQTASDKAIVNQDDETIVRLAEAGKAEIVP-- 243

Query: 233 SFGLNKPDKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLP 292
 F ++K + G +D + F + +LP+ E+ + GAHN N G
 Sbjct: 244 -FSVSKTLEQ--GAYVKDSM--IMFNGEAILPLEEVVLPGAHNLENILAAIAVVKTAGAS 298

Query: 293 FDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLA 352
 +A+ L +F+G+ HR Q+V G +Y+DSKATN+ D ++LLA
 Sbjct: 299 NEAVKKVLTSFTGVKHLRQYVTTVNGRKFYNDKATNILATSKALSA----FDKPVILLA 354

Query: 353 GGDGKGADFHDLPREPVARFCRAVVLLGRDAGLIAQALGNAVPLV--RVATLDEAVRQAA 409
 GG +G F DL+ P + +AV+ G+ A + + LGN + + RV +++AV A
 Sbjct: 355 GGLDRGNGFDDLK-PYMKHVKAVLTFGQTAPKL-EKLGNELGIQHVKRVNDNEQAVSAAF 412

Query: 410 ELAREGDAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
 L+ EGD +LLSPACAS D FK FEERG +F AV L
 Sbjct: 413 ALSNEGDVILLSPACASWDQFKTFEERGDMFIDAVHML 450

sp Q9K9S8 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 450
 MURD_BACHD 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Bacillus
 halodurans]

Score = 201 bits (510), Expect = 3e-50
 Identities = 142/446 (31%), Positives = 221/446 (48%), Gaps = 19/446 (4%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V+GL KSG + R L G V D + + Q + V CGE L
 Sbjct: 13 LVLGLAKSGEAAARLLHDLGAIVTVNDQKPLADNPQAQKLQKEGIHVVCGEHPISLLDGK 72

Query: 71 RELYVSPGLSLRTPALVQAAAGVRIISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
 + +PG+ P + +A +G+ + +++L ++ +A IVAITGSN K+T T+LV EM
 Sbjct: 73 ELVVKNPGIRYDNPIVEEAIKRGISVVTEVELASKVSEAEIVAITGSNGKTTTTSLVVEM 132

Query: 131 AVAADKRVAVGGNLTGTPALDL----LADDIELYVLELSSFQLETCDRNLNAEVATVLNVSE 186
 + + V GN+G A D+ ADD+ V+E+SSFQL +VA +LN+ +
 Sbjct: 133 LKGSAREPKVAGNIGVVASDVAREATADDV--IVMEVSSFQLMGTSHFRPKVAILLNIFD 190

Query: 187 DHMDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADTVPCWSFGLNKPDKFA 243
 H+D + +Y AK +I ++ V N D L + A+T K+
 Sbjct: 191 AHLDYHGSKENYVAAKKKIVENMKEEDYFVYNADDPLVSKVAAETKATPIPFSTRSTVVK 250

Query: 244 FGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAF 303
 + DG+ ++ F+ +K++ G++ + G HN N +G + + L F
 Sbjct: 251 GAYV--DGETYM-FRGEKIVEKGDVVLPGDHNVNDVLAAMSAALLMGATKEQIHVVLSTF 307

Query: 304 SGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHD 363
 SG+ HR Q+V +Y+DSKATN+ I VLLAGG +G F D
 Sbjct: 308 SGVEHRLQFVGTAFERKWYNDKATNILSTTAAIQSFTDPI---VLLAGGLDRGNSFDD 363

Query: 364 LREPVARFCRAVVLLGRDAGLIAQALGNA--VPLVRVATLDEAVRQAAELAREGDAVLLS 421
 L P + +AVVL G +AQA A +V +++AVR+A +++ GD +LLS
 Sbjct: 364 L-IPALQKVKAVVLFGETKHKLAQAAMEAGVETIVEAERVEDAVRKALDVSANGDVILLS 422

Query: 422 PACASLDMFKNFEERGRLFAKAVEEL 447
 PACAS D ++ FEERG F ++E L

Sbjct: 423 PACASWDQYRTFEERGEAFVTSIEGL 448

trnew CAE80955 **MurD protein (EC 6.3.2.9) [MURD] [Bdellovibrio** 462
bacteriovorus] AA
align

Score = 198 bits (504), Expect = 1e-49
Identities = 140/456 (30%), Positives = 221/456 (47%), Gaps = 29/456 (6%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRC---GELDAEFL 67
+VVGLGK+G+SL +L + G V D ++ PEL+ Q ++ ++ G F+
Sbjct: 14 LVVGLGKTGVSLAHFLT KHGAQVTVTD-HKSKPELSVQLEQLGELPIKFELGGHSPKTFI 72

Query: 68 CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
A++L + SPG+ A ++G++I+G+ + A K PI+ +TG+N K+TV +
Sbjct: 73 --AQDLVILSPGVPSNLKIFDYARSQGIKITGEFEFSAGFIKEPII GLTGTNGKTTVAKI 130

Query: 127 VGEMAVAADKRVAVGGNLTGPALDLLA--DDIELYVLELSSFQLETCDRNLNAEVATVLNV 184
+ + + VGG P +D L D ++ + E+SSF LE CD N N+
Sbjct: 131 TEAILTESGVKWTWVGANEKPLVDYLRLDDKAQVVI AEVSSFMLEHCDTFNPGNIVFTNL 190

Query: 185 SEDHMDRYDGMADYHLAKHRIFRGARQV---VVRADALTRPLIADTVPCWSFG----- 235
+E+H+DRY M +Y AK RIF+ Q ++N D L D P G
Sbjct: 191 AENHLDRYRSMEEYVNAKRRIFKNTNQATTSILNADDNAVVELARD--PAVQRGRIFYFS 248

Query: 236 ---LNKPDFKAFGLIEEDGQKWLAFQFDKL--LPVGELKIRGAHNYSNXXXXXXXXXGHAVG 290
+P G G + ++ + +K+RG H+ N G
Sbjct: 249 RKPALPQIMNIGGAVNIGDEIRVRTGPEIESFNIKGMKMRGKHSVENIMAAILASREHG 308

Query: 291 LPFDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVL 350
+A+ + F+GL HR ++VR+ GV +Y+DSKATNV D ++L
Sbjct: 309 ATREAVQKVINTFTGLPHRIEYVRKVGVGMFYNDKATNVHAVLRALDT---FDENVIL 364

Query: 351 LAGGDGKGADFHDREPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAE 410
+AGG ++ LR V R + ++L+G I + LG+ + T +EAV A +
Sbjct: 365 IAGGKDTNLNIEPLRTSVKRKVKTLILVGEAKERINRDLGDFSETFLIGTFEEAVLIAYQ 424

Query: 411 LAREGDAVLLSPACASLDMFKNFEERGRLFAKAVEE 446
+R GD VLLSP C+S DMF +FEERG F + V +
Sbjct: 425 KSRIGDVLLSPGCSSFDMFDSFEERG DYFKEIVRK 460

sp Q8KGD2 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC** 465
MURD_CHLTE **6.3.2.9)** AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Chlorobium
tepidum]

Score = 196 bits (498), Expect = 6e-49
Identities = 158/465 (33%), Positives = 227/465 (47%), Gaps = 42/465 (9%)

Query: 12 VVGLGKSGMSLVRYLARRGL-PFAVVDTRENPPELATLRAQYPQVEVRCGELD-AEFLCS 69
V+G GKSG+S LAR G PF +P ATLR Q+ V E +E +
Sbjct: 13 VIGAGKSGVSAAGLLARAGARPFLEFGAVSPEAAATLR---QLGVPFEEGGHSESVFE 68

Query: 70 ARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129
 A VSPG+ P + + A+G+ + +I+L + A I+ ITG++ K+T TL+
 Sbjct: 69 AALCIVSPGIPQTPVPIREMHARGIPVSEIELASWFCPARIIGITGTDGKTTTATLLHR 128

Query: 130 MAVAADKRVAVG----GNLGTPLD----LLADDIELYVLELSSSQLETCDRLNAEVATV 181
 + A +R GN+G P + A DI VLELSS+QLE C +A +
 Sbjct: 129 ICAAEGERKGFRAFSVGNIGIPFSSEVPGMTAADIA--VLELSSYQLEACFDPRPNIAVL 186

Query: 182 LNVSEDHMDRYDGMAD-YHLAKHRIFRGARQ-----VVVNRADALTRPLIADTVPCWSFG 235
 NV+ DHMDRY G + Y AK+RI ARQ ++ N D + R + P W F
 Sbjct: 187 TNVTPDHMDRYGGSIEAYATAKYRIH--ARQGAGDTLIYNHDDPILRAHFDRSEP-WPFR 243

Query: 236 LNKPDFKAFGL-----IEEDGQKWL--AFQFDKLLPVGELK---IRGAHNYSNXXXX 282
 L + +A L EDG+ + + ++L+ V E+ RG HN N
 Sbjct: 244 LVRLGLRAETLDVAPGDFVSVEDGEIVVRASGSTERLMRVDEIMKPGFRGEHNLNALSS 303

Query: 283 XXXGHAVGLPFDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXX 342
 A G+ + M G L F G+ HR + G+++ +DSKAT+V
 Sbjct: 304 VAAALAAGVAPETMRGVLAGFGGVEHRQELAGNACGLNWINDSKATSVNALRQALQS--- 360

Query: 343 DIDGKLVLLAGGDGKGADFDHDLREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLD 402
 + +VL+AGG KG D+ + + V +V +G IA A P+V A+L
 Sbjct: 361 -VPAGMVLIAGGRDKGNDYSAIADLVREKVACIVAIGESRRKIADAFRGVTPVVEAASLA 419

Query: 403 EAVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
 EAV A + AR G +VL SPAC+S DMF++FE+RGR F + V EL
 Sbjct: 420 EAVELARQNARPGASVLFSPACSSFDMFRDFEDRGRQFKQLVREL 464

sp Q8UDM6 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 469
 MURD_AGRT5 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Agrobacterium
 tumefaciens (strain C58 / ATCC 33970)]

Score = 190 bits (483), Expect = 4e-47

Identities = 151/454 (33%), Positives = 216/454 (47%), Gaps = 33/454 (7%)

Query: 14 GLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSAREL 73
 GLG SG+ R L G AVV +NP +A +A+ + +L S
 Sbjct: 16 GLGGSGLVATARALVAGGA--AVVAFDDNPDSVAKAQAE----GIATADLHTIDWSSFSSSF 69

Query: 74 YVSPGLSLRTP----ALVQAAAKGVRISGDIDLFAREAKA-----PIVAITGSNAKSTVT 124
 ++PG+ L P ++ A A GV + GDI+LF RE + P +AITG+N KST T
 Sbjct: 70 VLAPGVPLTHPKPHWSVDLAKAAGVEVIGDIELFIRERRVHAPDCPFIAITGTNGKSTTT 129

Query: 125 TLVGEMAVAADKRVAVGGNLTPLDILLADDIE-LYVLELSSSQLETCDRLNAEVATVLN 183
 L+ + ++ + +GGN+GT L L + YV+E SS+Q++ +N +LN
 Sbjct: 130 ALIAHILQSSGRDTQLGGNIGTAVLSLDPKQRFYVVECSSYQIDLAPTINPTAGILLN 189

Query: 184 VSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFG---LNKPD 240
 ++ DH+DR+ M Y K R+ G+ +V D+ + LIAD + ++K +
 Sbjct: 190 LTPDHLDRHGTMQHYADVKERLVAGSGTAIVGVDDSHST-LIADRIERAGVKVERISKRN 248

Query: 241 FKAFLIEEDGQKWLAQFDKLLPV---GELKIRGAHNYSNXXXXXXXXGHAVGLPFDAML 297

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      + GL E Q A      L V G      +RG+HN N      AVG+ + +
Sbjct: 249 VVSEGLYAEGSQILRAHGGTSSLLVDLDGIQTLRGSHNAQNAAAAIAACLAVGVSEEEIR 308

Query: 298 GALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGK 357
      LK+F GL HR Q V R V++ +DSKATN      ++ +AGG K
Sbjct: 309 AGLKSFPGLKHRMQPVGRRGNVTFVNDSKATNADAAAPALSSF-----DRIYWIAGGLPK 363

Query: 358 GADFHDLREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELARE--- 414
      L      R +A L+G A A LG AVP      TLD+AV+ AA A +
Sbjct: 364 AGGITSLSPFLFPRIAKA-YLIGEAFAAFAATLGEAVPYEISGTLDKAVQHAAADA EKDAT 422

Query: 415 -GDAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
      G+ V+LSPACAS D +KNFE RG F V L
Sbjct: 423 AGNVVMLSPACASFDQYKNFEIRGDSFVAQVAAL 456

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tr Q7NEZ5 UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]      441
      [Gloeobacter
      violaceus]      AA
                        align

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Score = 190 bits (482), Expect = 5e-47

Identities = 149/448 (33%), Positives = 212/448 (47%), Gaps = 24/448 (5%)

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Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYP-QVEVRCGELDAEFLCSA 70
      VVG GKSG + R+LA G + D R++      A P VE G EF+
Sbjct: 6 VVGAGKSGQAAARWLALGRRVVLWDGRDSEALRVVAGALAPFGVEAVLGR---EFVPEE 62

Query: 71 REL---YVSPGLSLRTPALVQAAKGVRISGDIDL-FAREAKAPIVAITGSNAKSTVTTL 126
      +L VSPG+ P LV A A+GV ++G++ L + + +TG+N K+T T L
Sbjct: 63 PDLISLVVSPGVRWDHPGLVAARARGVTVTGEVGLAWESLSHRRWLCVTGTNGKTTTAL 122

Query: 127 VGEMAVAADKRVAVGGNLGTPLDALLAD--DIELYVLELSSFQLETCDRLNAEVATVLNV 184
      VG + A R V GN+G P DLL + D + V ELSSFQ+E+ + EVA
Sbjct: 123 VGHILKTAGLRAPVCGNIGRPVTDLLLEPEDYDWIVAEELSSFQIESAQGIRPEVAVWTTF 182

Query: 185 SEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPDKAF 244
      + DH++R+ + Y K + AR+ V+N DA + W P A
Sbjct: 183 TPDHLNRHGTLERYAAIKAGLLMQARRAVLNGDDAYLGARRSAWPDAAWTSTQAP--AAV 240

Query: 245 GLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFS 304
      L +D + + +LPV +++ GAHN N H G+ A+ + +F
Sbjct: 241 SLAGKD---ICIENRPVLPVSAVRLPGAHNLQNVLMAVAACHLTGVGDAAIASGVASFI 296

Query: 305 GLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDL 364
      G+ HR + V E +GV + +DSKATN + VL+AGG K +
Sbjct: 297 GVPHRLEAVGEYRGVRFINDSKATNYDAALVGLTA----VPAPSVLIAGGQAKTGESGPW 352

Query: 365 REPVARFCRAVVLLGRDAGLIAQAL--GNAVPLVRVATLDEAVRQAAELAREGDA--VLL 420
      +A C +VVL+G A L + L + + TL+ AV A E AR A VL
Sbjct: 353 LRAIAERCASVVLIGEAAPLFEKWLRAQDYRAVYTAHTLERAVPMAFEQARAQGAQCQLF 412

Query: 421 SPACASLDMFKNFEERGRLFAKAVEELA 448
      SPACAS D F+NFEERG F + LA
Sbjct: 413 SPACASFDQFRNFEERGDRFRALIAALA 440

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sp Q8DMN8 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 454**
 MURD_SYNEL **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) **align**
(D-glutamic acid adding enzyme) [MURD] [Synechococcus
elongatus (Thermosynechococcus elongatus)]

Score = 189 bits (479), Expect = 1e-46

Identities = 142/457 (31%), Positives = 218/457 (47%), Gaps = 29/457 (6%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPP---ELATLRAQYPQVEVRCGELDAEFLC 68
 V+GLG+SG++ R L R+G V D R+ P + L+A+ V++ + D + L
 Sbjct: 6 VIGLGRSGIAAARLLKRQGWQVEVSDRRQTPALQSQQQLQAEGIPVQLNY-DFDLQTLI 64

Query: 69 SAR-----ELYVSPGLSLRTPALVQAAAKGVRISGDIDL-FAREAKAPIVAITGSNAKST 122
 S E+ +SPG+ +PALV A G+ + G++ + + A P V ITG+N K+T
 Sbjct: 65 SVGLRVPDEIVISPGVPWHSPALVAARQAGIPVRGEVAIAWQTLAHLPPWCITGTNGKTT 124

Query: 123 VTTLVGEMAVAADKRVAVGGNLTGPALD--LLADDIELYVLELSSSFQLETCDRLNAEVAT 180
 T L + AA GN+G + L A ++ + E+SS+QLE+ L E A
 Sbjct: 125 TTALTAALFQAAGYNAPACGNIGNSICEVALTARALDWVIAEISSYQLESSPPLQPEFAL 184

Query: 181 VLNVEDHMDRYDGMADYHLAKHRIFRGARQVVNRADALTRPLIADTVP-CWSFG---- 235
 ++ DH++R+ + Y K + GA+ V++N D R + + P W
 Sbjct: 185 WTTLTDPDHLERHGTLDAYVATKAHLMNGAKHVILNGDDPYLRQHMVNRWPQAWWISTQGA 244

Query: 236 LNKPDFKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNSNXXXXXXXXXGHAVGLPFDA 295
 + P A G+ + Q W FQ LLP L++ G HN N H G+P +
 Sbjct: 245 IALPKGIAQGIYIAEDQVW--FQDQPLLPHTILQMPGRHNQQNFLLAVATAHLAAGIPAET 302

Query: 296 MLGALKAFSGLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGD 355
 + + F+G+ HR + +R+ + V + +DSKATN + G ++L+AGG
 Sbjct: 303 IAKGVAGFAGVPHRLERIRQWREVIEWINDSKATN----YDAAEIGLRSVTGPVILIAGGQ 358

Query: 356 GKGADFDHDLREPVARFCRAVLLGRDAGLIAQALGNAVPLVR---VATLDEAVRQAAELA 412
 K D + V+L+G A AQ L A+ + TLD AV AAEL
 Sbjct: 359 AKKGDDRPWLNLIQEKAAWVLLIGEAPQFAQRL-EAIGFTNYEIMETLDRAVAAAELV 417

Query: 413 REG--DAVLLSPACASLDMFKNFEEGRGLFAKAVEEL 447
 + VL SP CAS D ++NFEERG F + EL
 Sbjct: 418 TQYPIKTVLFSPGCASFQYQNFEEGRGDHFRQLCLEL 454

sp Q9A597 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 471**
 MURD_CAUCR **6.3.2.9)** **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) **align**
(D-glutamic acid adding enzyme) [MURD] [Caulobacter
crescentus]

Score = 187 bits (475), Expect = 3e-46

Identities = 150/465 (32%), Positives = 219/465 (46%), Gaps = 46/465 (9%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPPELATLRAQYPQVEVRCGELDAEFLCSAR 71
 V GLG++G++ R L G A+ D + E A + V+++ + ++F
 Sbjct: 14 VFGLGRTGLTAARALIAGGAKVALWDEKPASREAAAEG-FAVVDLQAADW-SQFAA--- 68

Query: 72 ELYVSPGLSLRTP----ALVQAAAKGVRISGDIDLFAREAKAP-----IVAITGSNAK 120
 L +SPG+ L P + +A A GV + GD++LFAR A I+AITG+N K

Sbjct: 69 -LMLSPGVPLSHPKPHWTVVEKARAAGVEVLGDVELFARTVNAAPAHKRPKIIAITGTNGK 127

Query: 121 STVTTLVGEMAVAADKRVAVGGNLTGTPALDLLADDIE---LYVLELSSSFQLETCDRLNAE 177
ST T L+G + +A + VGGN+G L L +D+ +YVLELSS+QL+ L +

Sbjct: 128 STTTALIGHLCASAGRDTRVGGNIGLGVGL--EDMHGGAVYVLELSSYQLDLTSSLKPD 185

Query: 178 VATVLNVSEDHMDRYDGMADYHLAKHRIF--RGARQVVVNRAAD-----ALTRPLIADTV 229
+LN+S DH+DR+ GM Y AK RIF +G + D T A+

Sbjct: 186 AVVLLNISPDHLDRHGGMDGYIAAKRRIFLNQGGKDTAIGVDDAWCQQICTEITAANRR 245

Query: 230 PCWSFGLNKPDKFAFGLIEEDGQKWLAFQFDKLLPVGEL---KIRGAHNYSNXXXXXXX 285
W K G+ G + A ++++ V ++ + G HN+ N

Sbjct: 246 TIWPISAGKA--MGRGVYALQGVLYDA-TGERVVEVADILRARSPLGRHNWQNAAYAA 302

Query: 286 GHAVGLPFDAMLGALKAFSGLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDID 345
A+G+ + L F GLAHR + V + V + +DSKATN

Sbjct: 303 ARAIGISMQDAVDGLMTFPGLAHRMETVGKIGKVRVFNDSKATNADAARQAMSSY----- 357

Query: 346 GKLVLLAGGDKGADFDHDLREPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDEAV 405
K +AGG K DL++ R +A L+G A + L V TL++AV

Sbjct: 358 PKFYWIAGGVAKAGGIDDLKDLFPRIAKA-YLIGEAAEPFSWTLAGKAECVLSGTLEKAV 416

Query: 406 RQA-AELAREGD--AVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
+QA A+ A G+ VLLSPACAS D F +FE RG F AV L

Sbjct: 417 QQAYADAAASGEEAIVLLSPACASFDQFSDFEARGEAFRAAVNGL 461

sp Q8E6P1 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC** 451
MURD_STR43 **6.3.2.9)** AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Streptococcus
agalactiae (serotype III)]

Score = 184 bits (467), Expect = 3e-45

Identities = 135/456 (29%), Positives = 225/456 (48%), Gaps = 39/456 (8%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVDTR---ENPPELATLRAQYPQVEVRCGE-----L 62
+V+GL +SG + R LA+ G V D + ENP + L ++V CG L

Sbjct: 13 LVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEG---IKVVCGSHPLELL 69

Query: 63 DAEFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKST 122
D +F + +PG+ P + +A K + + +++L +++ ++ ITGSN K+T

Sbjct: 70 DEDFCYMIK---NPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIGITGSNGKTT 125

Query: 123 VTTTLVGEMAVAADKRVAVGGNLTGTPALDLL--ADDIELYVLELSSSFQLETCDRLNAEVAT 180
TT++ E+ A +R + GN+G PA +++ ADD ++ V+ELSSFQL +A

Sbjct: 126 TTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDILVMELSSFQLMGVKEFRPHIAV 185

Query: 181 VLNVEDHMDRYDGMADYHLAKHRI---FRGARQVVVNRAADALTRPLIADTVPCWSFGLN 237
+ N+ H+D + DY AK I + +V+N +++ L T

Sbjct: 186 ITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFVLVNFNQISKELAKTT----- 236

Query: 238 KPDKFAFGLIEE-DG----QKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLP 292
K F E+ DG K L ++ + ++ V ++ + G+HN N G+

Sbjct: 237 KATIVPFSTTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGIS 296

Query: 293 FDAMLGALKAFSGLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXIDGKLVLLA 352
 + L F G+ HR Q + + G+S+Y+DSK+TN+ + K++L+A
 Sbjct: 297 NQVIRETLNFGGVKHLRLQSLGKVHGISFYNSKSTNILATQKALSGFD---NTKVILIA 353

Query: 353 GGDGKGADFHDLEPVARFCRAVLLGRDAGLIAQALGNA-VPLVRVATLDEAVRQAAEL 411
 GG +G +F +L + + +V+LG A + +A A V + +AV +A E+
 Sbjct: 354 GGLDRGNEFDELIPDITGL-KHMMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEV 412

Query: 412 AREGDAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
 A++GD +LLSPA AS DM+KNFE RG F E L
 Sbjct: 413 AQQGDVILLSPANASWDMYKNFEVRGDEFIDTFESL 448

tr Q8A256 **UDP-N-acetylmuramoylalanine--D-glutamate ligase** 413 AA
[BT3450] align
[Bacteroides thetaiotaomicron]

Score = 183 bits (465), Expect = 4e-45
 Identities = 130/405 (32%), Positives = 205/405 (50%), Gaps = 30/405 (7%)

Query: 60 GELDAEFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNA 119
 G E + +A E+ SPG+ P +++ A+G + +I+ R A ++ ITGSN
 Sbjct: 22 GHTEELILNADEVIKSPGIPNDAPLILKLKAQGTPVISEIEFAGRYTDAKMICITGSNG 81

Query: 120 KSTVTTLVGEMAVAADKRVAVGGNLG-TPALDLLADDIELYVLELSSFQLETCDRLNAEV 178
 K+T T+L+ + +AD V + GN+G + AL + + + Y++ELSSFQL+ A +
 Sbjct: 82 KTTTSLIYHIFKSADLNVGLAGNIGKSLALQVAEEHHDYIIEELSSFQLDNMYNFRANI 141

Query: 179 ATVLNVSEDHMDRYDG-MADYHLAKHRIFRGAR---QVVVNRADALTRPLIADTVPCWSF 234
 A ++N++ DH+DRYD M +Y AK RI + + D + + +A
 Sbjct: 142 AVL MNITPDHLDHYDHCMQNYIDAKFRITQNQTDDAFIFWDDPIIKQELA-----KH 195

Query: 235 GLNKPDKFAFLIEEDGQKWLAFQFDKLLPV-----GELKIRGAHNYSNXXXXXX 284
 GL K F ++EDG +A+ D + + EL + G HN N
 Sbjct: 196 GL-KAHLYPFAAVKEDGA--IAYVEDHEVKITEPIAFNMEQEELALTGQHNLYNSLAAGI 252

Query: 285 XGHAVGLPFDAMLGALKAFSGLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDI 344
 + G+ + + AL F G+ HR + V +G+ + +DSKATNV
 Sbjct: 253 SANLAGITKENIRKALSDFKGVHRLEKVARVRGIDFINDSKATNVNSCWYALQSMTT-- 310

Query: 345 DGKLVLLAGGDGKGADFHDLEPVARFCRAVLLG-RDAGLIAQALGNAVPLVRVAT-LD 402
 K VL+ GG KG D+ ++ + V C A+V LG + L A +P+ V T +
 Sbjct: 311 --KTVLILGGKDKGNDYTEIEDLVREKCSALVYLGLHNEKLHAFDFRGLPVADVQTGMK 368

Query: 403 EAVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
 +AV A +LA++G+ VLLSP CAS D+FK++E+RG F K V EL
 Sbjct: 369 DAVEAAYKLAKKGETVLLSPCCASFDLFSYEDRGDQFKKYVREL 413

sp Q8E186 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC** 451
MURD_STRAS **6.3.2.9)** **(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)** AA
(D-glutamic acid adding enzyme) [MURD] [Streptococcus align
agalactiae (serotype V)]

Score = 182 bits (461), Expect = 1e-44

Identities = 134/456 (29%), Positives = 224/456 (48%), Gaps = 39/456 (8%)

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Query: 11  IVVGLGKSGMSLVRYLARRGLPFAVVDTR---ENPPELATLRAQYPQVEVRCGE-----L 62
      +V+GL +SG + R LA+ G V D + ENP + L ++V CG L
Sbjct: 13  LVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEG---IKVVCGSHPLELL 69

Query: 63  DAEFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKST 122
      D +F + +PG+ P + +A K + + +++L +++ ++ ITGSN K+T
Sbjct: 70  DEDFCYMIK---NPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQSLIGITGSNGKTT 125

Query: 123 VTTLVGEMAVAADKRVAVGGNLTGTPALDLL--ADDIELYVLELSSFQLETCDRLNAEVAT 180
      TT++ E+ A +R + GN+G PA +++ A+D + V+ELSSFQL +A
Sbjct: 126 TTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELELSSFQLMGVKEFRPHIAV 185

Query: 181 VLNVEDHMDRYDGMADYHLAKHRI---FRGARQVVNRADALTRPLIADTVPCWSFGLN 237
      + N+ H+D + DY AK I + +V+N +++ L T
Sbjct: 186 ITNLMPTHLDYHGSFEDYVAAKWNIQNMSSDFLVLFNFGISKELAKTT----- 236

Query: 238 KPDKFAFLIEE-DG----QKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXGHAVGLP 292
      K F E+ DG K L ++ + ++ V ++ + G+HN N G+
Sbjct: 237 KATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGIS 296

Query: 293 FDAMLGALKAFSGLAHRQCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLA 352
      + L F G+ HR Q + + G+S+Y+DSK+TN+ + K++L+A
Sbjct: 297 NQVIRETLNFGGVKHLRLQSLGKVHGHSFYNDKSTNILATQKALSGFD---NTKVILIA 353

Query: 353 GGDGKGADFHDLREPVARFCRAVVLLGRDAGLIAQALGNA-VPLVVRVATLDEAVRQAAEL 411
      GG +G +F +L + + +V+LG A + +A A V + +AV +A E+
Sbjct: 354 GGLDRGNEFDELIPDITGL-KHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEV 412

Query: 412 AREGDAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
      A++GD +LLSPA AS DM+KNFE RG F E L
Sbjct: 413 AQQGDVILLSPANASWDMYKNFEVRGDEFIDTFESL 448

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sp Q8ER50      UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC      449
MURD_OCEIH 6.3.2.9)                                     AA
      (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)      align
      (D-glutamic acid adding enzyme) [MURD] [Oceanobacillus
      iheyensis]

```

Score = 180 bits (457), Expect = 4e-44

Identities = 133/448 (29%), Positives = 215/448 (47%), Gaps = 23/448 (5%)

```

Query: 11  IVVGLGKSGMSLVRYLARRGLPFAVVDTRENNPELATLRAQYPQVEVRCGELDAEFLCSA 70
      +V+GL KSG + L + + + D + + Q E+ G L
Sbjct: 13  LVLGLAKSGTAAANVLLQNHIQVTINDGMATLEDATVQKLQTMGAELVLGSHPISVLDGK 72

Query: 71  RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTTLVGEM 130
      + +PG+ + +A +G+ + +++L P++ ITGSN K+T TTL+ EM
Sbjct: 73  DLIVKNPGIRYDNIIVIEEAQRRGIPVISEVELVHYLTNPVIGITGSNGKTTTTTTLITEM 132

Query: 131 AVAADKRVAVGGNLTGTPALDLLA--DDIELYVLELSSFQLETCDRLNAEVATVLNVSEDH 188
      ++ V V GN+G A ++ + E V+ELSSFQL+ D+L A +LN+ E H
Sbjct: 133 LDRSNVSVKVAGNIGVVATEVASSLQSDKMMELSSFQLOGIDQLQFSTAVLLNLFEAH 192

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Query: 189 MDRYDGMADYHLAKHRIFRGARQ---VVVNRAD----ALTRPLIADTVPCWSFGLNKPDPF 241
 +D + +Y AK IF+ + ++ N D A + A VP F ++P
 Sbjct: 193 LDYHGSFENYVEAKCNIFKSQNKHDYLIYNADDDNVSAAIKTAEATKVP---FSSSRP-- 247

Query: 242 KAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALK 301
 A G +D +L ++ +K++ + ++ + G HN N G + ++ L
 Sbjct: 248 LADGAWMDD--DFLYYKDEKIIAIRDIVLVGKHNMENILAAIATAKLNGATNEGIVQVLT 305

Query: 302 AFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADF 361
 FSG+ HR ++V G Y+DSKATN+ ++ VLLAGG +G F
 Sbjct: 306 TFSGVKHRLEFVGVIINGRYIYNDKATNILATKKALAAFNKNV----VLLAGGLDRGNTF 361

Query: 362 HDLREPVARFCRAVVLLGRDAGLIAQA-LGNAVPLVRVA-TLDEAVRQAAELAREGDAVL 419
 +L P +A+V+ G AG + A + +P++ A + AV A L E D +L
 Sbjct: 362 EEL-IPYLHHVKAMVVFGETAGKLKDAGVAANIPVIEKALDVQHAVEVAFALTDEQDTIL 420

Query: 420 LSPACASLDMFKNFEERGRLFAKAVEEL 447
 LSPACAS D +K FEERG +F +A+ L
 Sbjct: 421 LSPACASWDQYKTFEERGDMFIQALHRL 448

sp Q8YI68 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 467
 MURD_BRUME 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Brucella
 melitensis]

Score = 179 bits (455), Expect = 6e-44

Identities = 150/458 (32%), Positives = 210/458 (45%), Gaps = 46/458 (10%)

Query: 14 GLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSAREL 73
 GLG SG++ + + G D +NP +A RAQ + G+L
 Sbjct: 16 GLGGSGIATAKAIVAGGARIIAWD--DNPDSVA--RAQ--SAGIATGDLRQADWSQFAVF 69

Query: 74 YVSPGLSLRTP----ALVQAAAKGVRISGDIDLFAREAK-----APIVAITGSNAKSTVT 124
 +SPG+ L P ++ A A GV I GD++LF RE P +AITG+N KST T
 Sbjct: 70 VLSPGVPLTHPQPHWSVDLARAAGVEIIGDVLEFVREERNHIAPDCPFIAITGTNGKSTTT 129

Query: 125 TLVGEMAVAADKRVAVGGNLGTPALDL-LADDIELYVLELSSFQLETCDRLNAEVATVLN 183
 L+ + A + + +GGN+GT L L L YV+E SS+Q++ LN +LN
 Sbjct: 130 ALIAHIIKATGRDMQLGGNIGTAILTLELPCADRFYVVECSSYQIDLAPSLNPTAGILLN 189

Query: 184 VSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPDPFKA 243
 ++ DH+DR+ M +Y K R+ + ++ DA + IAD L+ +
 Sbjct: 190 LTPDHLDRHGSMENYAAIKERLVAASGTAIIGIDDAYCQA-IADR-----LHGAGIRV 241

Query: 244 FGLIEE-----DGQKWLAQFDKLLPVGELK---IRGAHNYSNXXXXXXXXXGHAVG 290
 + +E DG K L Q ++ + L+ +RGAHN N + G
 Sbjct: 242 VRISKEKHLDRGYFADGAKLLWAQDGEIDEIASLEGIGSLRGAHNAQNALAAIVACLSAG 301

Query: 291 LPFDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVL 350
 L + + LK+F GLAHR + V R V + +DSKATN +I
 Sbjct: 302 LSLEEIHAGLKSFPGLAHRMEQVGRGKVLVFNDSKATNAEATAPALSSFPQNI----YV 357

Query: 351 LAGGDGKGADFHDREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAE 410

+ GG K + L R +A L+G A A LG AVP TL AV AA
Sbjct: 358 IVGGVPKAGGINSLTAFFPRVAKA-YLIGEAAAQFAATLGGAVPFEISDTLAAAVAHAAG 416
Query: 411 LAREGDA----VLLSPACASLDMFKNFEERGRLFAKAV 444
A A VLLSPACAS D F+NFE+RG F AV
Sbjct: 417 DAGNDAAPEPVVLLSPACASFDQFQNFEEKRGDAFRDAV 454

sp Q8FZP2 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 467
MURD_BRUSU 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Brucella suis]

Score = 179 bits (454), Expect = 8e-44
Identities = 151/460 (32%), Positives = 211/460 (45%), Gaps = 50/460 (10%)

Query: 14 GLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSAREL 73
GLG SG++ + + G D +NP +A RAQ + G+L
Sbjct: 16 GLGGSGIATAKAIVAGGARIIAWD--DNPDSVA--RAQ--SAGIATGDLRQADWSQFAVF 69
Query: 74 YVSPGLSLRTP----ALVQAAAKGVRISGDIDLFAREAK-----APIVAITGSNAKSTVT 124
+SPG+ L P ++ A A GV I GD++LF RE P +AITG+N KST T
Sbjct: 70 VLSPGVPLTHPQPHWSVDLARAAGVEIIGDVELFVRERNHIAPDCPFIAITGTNGKSTTT 129
Query: 125 TLVGEMAVAADKRVAVGGNLTGTPALDL--LADDIELYVLELSSFQLETCDRLNAEVATV 181
L+ + A + + +GCN+GT L L AD YV+E SS+Q++ LN +
Sbjct: 130 ALIAHIIKATGRDMQLGGNIGTAILTLEPPCAD--RFYVVECSSYQIDLAPSLNPTAGIL 187
Query: 182 LNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVN RADALTRPLIADTVPCWSFGLNKPDPF 241
LN++ DH+DR+ M +Y K R+ + ++ DA + IAD L+
Sbjct: 188 LNLTPDHLDRHSGMENYAAIKERLVAASGTAIIGIDDAYCQA-IADR-----LHGAGI 239
Query: 242 KAFGLIEE-----DGQKWLAQFDKLLPVGELK----IRGAHNYSNXXXXXXXXXGHA 288
+ + +E DG K L Q ++ + L+ +RGAHN N +
Sbjct: 240 RVVRISKEKHLDRGYFADGAKLLWAQDGEIDEIASLEGIGSLRGAHNAQNALAAIVACLS 299
Query: 289 VGLPFDAMLGALKAFSGLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKL 348
GL + + LK+F GLAHR + V R V + +DSKATN +I
Sbjct: 300 AGLSLEEIHAGLKSFPGLAHRMEQVGRGKVLVFNDSKATNAEATAPALSSFPQNI---- 355
Query: 349 VLLAGGDGKGADFHDLEPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQA 408
+ GG K + L R +A L+G A A LG AVP TL AV A
Sbjct: 356 YWIVGGVPKAGGINSLTAFFPRVAKA-YLIGEAAAQFAATLGGAVPFEISDTLAAAVAHA 414
Query: 409 AELAREGDA----VLLSPACASLDMFKNFEERGRLFAKAV 444
A A A VLLSPACAS D F+NFE+RG F AV
Sbjct: 415 AGDAGNDAAPEPVVLLSPACASFDQFQNFEEKRGDAFRDAV 454

sp Q8DVE3 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 451
MURD_STRMU 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Streptococcus
mutans]

Score = 177 bits (450), Expect = 2e-43

Identities = 137/448 (30%), Positives = 219/448 (48%), Gaps = 23/448 (5%)

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Query: 11  IVVGLGKSGMSLVRYLARRGLPFAVVDTR---ENPPELATLRAQYPQVEVRCGELDAEFL 67
      +V+GL +SG +  R LA+ G      V D +  ENP  A L      ++V CG      E L
Sbjct: 13  LVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPSAQALLEEG---IKVICGSHPLELL 69

Query: 68  CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
      A      V +PG+      P +V+A  K + +  +++L      ++API+ ITGSN K+T TT+
Sbjct: 70  DEAFAYMVKNPPIPYPYTNPMVVRALEKNIPVITEVELAYLISEAPIIGITGSNGKTTTMT 129

Query: 127  VGEMAVAADKRVAVGGNLTGPALDLL--ADDIELYVLELSSFQLETCDRLNAEVATVLNV 184
      + ++  A +      + GN+G PA ++      + ++ V+ELSSFQL  + +  +A + N+
Sbjct: 130  IADVLNHAGQSARLSGNIGFPASEVAQPVTEKDILVMELSSFQLMGTESFHPHMAVITNL 189

Query: 185  SEDHMDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADT-VPCWSFGLNKP 240
      H+D +      +Y AK I +      + +V+N      L + L  T      F +
Sbjct: 190  MPTHIDYHGSFENYIEAKWNIQKNMTKEDFLVLNFNQDLAKDLANQTQAKIIPFSTKEKV 249

Query: 241  FKAFLIEEDGQKWLAQFDKLLPVGELKIRGAHNSNXXXXXXXXXGHAVGLPFDAMLGAL 300
      A+      DGQ L F+      ++  EL + G+HN N      G+ +A+  L
Sbjct: 250  DGAY----LDGQM-LCFKGQAIMSASELGVPGSHNVENALATIAVAKLSGVSNEAIRETL 304

Query: 301  KAFSGLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
      F G+ HR Q +      GV +Y+DSK+TN+      + K++L+AGG  +G +
Sbjct: 305  IHFGGVKHLRLQSLGNIAGVKFYNDKSTNILATQKALSGFD---NSKVILIAGGLDRGNE 361

Query: 361  FHDLREPVARFCRAVLLGRDAGLIAQALGNA-VPLVRVATLDEAVRQAABELAREGDAVL 419
      F +L P +      + +++LG A + A  A V +      + +A R A + A  GD VL
Sbjct: 362  FDEL-VPDIKGLKKMIILGESAPRLKHAHVQAGVTYLNKADVAQATRIAFQEASPGDVVL 420

Query: 420  LSPACASLDMFKNFEERGRLFAKAVEEL 447
      LSPA AS DM+KNFE RG  F      + L
Sbjct: 421  LSPANASWDMYKNFEVRGDEFITTFKSL 448

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sp  Q97EB9      UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC      462
    MURD_CLOAB  6.3.2.9)                                     AA
                  (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)  align
                  (D-glutamic acid adding enzyme) [MURD] [Clostridium
                  acetobutylicum]

```

Score = 177 bits (449), Expect = 3e-43

Identities = 134/451 (29%), Positives = 220/451 (48%), Gaps = 23/451 (5%)

```

Query: 12  VVGLGKSGMSLVRYLARRGLPFAVVD--TRENPELATLRAQYPQVEVRCGELDAEFLCS 69
      VVG+G S  L+ +L++ G      D T+E  +      V+  GE      L
Sbjct: 19  VVGMGISNRPLIHFLSKLGAIEITAFDRKTKEELGDEVINEFSSENVKFELGENYLSALKG 78

Query: 70  ARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGE 129
      ++ +P + + + ALV+A  +G I+ +++ F +  A I  +TGS+ K+T TTL+
Sbjct: 79  FDVVFKTPSMRIDSEALVKAKQEGAYITSEMEEFIKYCPAKIFGVTGSDGKTTTTTTLIYN 138

Query: 130  MAVAADKRVAVGGNLTGPALDLLAD--DIELYVLELSSFQLETCDRLNAEVATVLNVSED 187
      M      + VGGN+GTP  + +      + VLELSSFQL T D ++ EVA V N+S +
Sbjct: 139  MLKEEGYKTWVGGNIGTPLFSKIKEVSTKDKVVLELSSFQLMTID-VSPEVAVVTNLSN 197

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Query: 188 HMDRYDGMADYHLAKHRIFRGARQ--VVVNRADALTRPLIADTV-PCWSFGLNKPDFKA 243
 H+D + M +Y AK IF + +++NR + +T + ++ + F N+

Sbjct: 198 HLDIHKNMEEYINAKKNIFTHQSKGNVLIINRDNEITNNMESEALGDLLKFSRNEKVKNG 257

Query: 244 FGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXGHAVGLPFDAMLGALKAF 303
 ++DG +L F+ +K+ ++KI+G N N + + ++M+ F

Sbjct: 258 AYYNKQDGNIIYL-FE-NKICNKDDIKIKGMDNVKN-FMAAFCAVSKDVSKESEMIKVAMNF 314

Query: 304 SGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHD 363
 +G+ HR ++VRE GV YY+DS A++ + ++L+AGG K F

Sbjct: 315 AGVEHRREFVRELDGVKYYNDSIASSPTRTISGLNA----YERPVLIIAGGYDKHIPFEP 370

Query: 364 LREPVARFCRAVVLLGRDAGLIAQALGNAV-----PLVRVATLDEAVRQAAELAREGD 416
 L E + ++L+G I + + P++ L+EAV +A ++A GD

Sbjct: 371 LAEKGYDKIKVLILMGATKNKIKETFDKVICEKNIKLPIILSDNLEEAVCEAKKVATNGD 430

Query: 417 AVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
 V LSPACAS D F NFE RG F + V L

Sbjct: 431 IVTLSPACASFDSFPNFVGRGNKFKEIVNNL 461

sp Q9CF91 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 450
 MURD_LACLA 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Lactococcus
 lactis (subsp. lactis) (Streptococcus lactis)]

Score = 176 bits (447), Expect = 5e-43

Identities = 135/449 (30%), Positives = 217/449 (48%), Gaps = 25/449 (5%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQY---PQVEVRCGELDAEFL 67
 +V+GL +SGM+ L G A+V + P AQ ++V G + L

Sbjct: 13 LVLGLARSGMAAALVLNELG---AIVTVNDGKPFEEENKEAQLLLEGIKVITGSHPIDLL 69

Query: 68 CSARELYV-SPGLSLRTPALVQAAAGVRIISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
 L V +PG+ P + +A A + + +++L ++API+ ITG+N K+T TTL

Sbjct: 70 DEDFALMVKNPGIRYDNPMVERAEALNIPVITEVELAYLISEAPIIGITGTNGKTTTTTL 129

Query: 127 VGEMAVAADKRVAVGGNLGTPALDLL--ADDIELYVLELSSFQLETCDRLNAEVATVLNV 184
 + ++ A + + GN+G PA ++ A + V+ELSSFQL D ++A + N+

Sbjct: 130 IADILNADGQSAKLSGNIGFPASEVAEKASASDTLVMELSSFQLMGIDSFRPKIALITNL 189

Query: 185 SEDHMDRYDGMADYHLAKHRIFRGARQ--VVVNRADALTRPLIADTVPCWSFGLNKPDF 241
 H+D + Y AK RI +++N R L AD + +

Sbjct: 190 FSAHLDYHGSQKAYEAAKWRIQENMTSDDFLILNFNQEKCRNL-ADKTKATVLAFASTKE- 247

Query: 242 KAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXGHAVGLPFDAMLGALK 301
 K G +DG+ + F + ++ V EL + G HN N G +A++ L

Sbjct: 248 KVNGAYS KDGK--IYFNDEYIMEVSELSLPGHNLENALAAIVASKLQGTKNEAIVEVLT 305

Query: 302 AFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADF 361
 +F+G+ HR Q++ E G Y+DSKATN+ + KL LLAGG +G F

Sbjct: 306 SFAGVKHRLQYLGEIDGRKQVYNDKATNILATQKALSGFD---NSKLWLLAGGLDRGNF 362

Query: 362 HDLREPVARFCRAVVLLGRDAG---LIAQALGNAVPLVRVATLDEAVRQAAELAREGDAV 418

```

      +L + + + + +V+ G+ A   L A+ L   +P+       + +A+ +       + GD +
Sbjct: 363 EELEKDL-QDLKGMVVFQGTANKLRLTAEKLN--IPVFDSENVAKALEEILPQTQAGDTI 419

Query: 419 LLSPACASLDMFKNFEERGRLLFAKAVEEL 447
      LLSPACAS D +K FEERG LF +A E L
Sbjct: 420 LLSPACASWDQYKTFEERGDLEFIQAFENL 448

```

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sp 007669      UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC      460
MURD_ENTHR 6.3.2.9) AA
      (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
      (D-glutamic acid adding enzyme) [MURD] [Enterococcus
      hirae]

```

Score = 176 bits (446), Expect = 7e-43

Identities = 145/452 (32%), Positives = 218/452 (48%), Gaps = 27/452 (5%)

```

Query: 11  IVVGLGKSGMSLVRYLARRGLPFAVVDTR--ENPPELATLRAQYPQVEVRCGELDAEFLC 68
      +V+GL KSG S + L G   V D + + PE L +   V+V G   E L
Sbjct: 17  LVLGLAKSGFSAAKLLHELGAULTVNDGKPFDEKPEAQELLSL--GVKVIAGSHPIELLD 74

Query: 69  SARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLV 127
      L V +PG+   P + +A G+ +   +++L   A+ PI+ ITG+N K+T TT+
Sbjct: 75  EEFSLMVKNPGIPYSHPFVQKAQELGIPVITEVELAYEVAECPIIGITGTNGKTTTTTMT 134

Query: 128 GEMAVAADK--RVAVGGNLGTPALDLL----ADDIELYVLELSSSFQLETCDRLNAEVATV 181
      G + A D   + GN+G PA +   ADD   V+ELSSFQL   VA V
Sbjct: 135 GLLLNAGDLPGTARLAGNIGYPASSVAQEATADD--KIVMELSSFQLMGITDFRPHVAVV 192

Query: 182 LNVSEDHMDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADT-VPCWSFGLN 237
      N+ E H+D +   +Y AK + + +   +++N   R L T   F
Sbjct: 193 TNIYEAHIDYHKTRKEYVKAQWHLQQNMTEKDYLILNWNQEELRELSKKTATVLPFATE 252

Query: 238 KPDFKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAML 297
      + K G   DG + + +K++ + EL + G+HN N   G+ +A+
Sbjct: 253 QKLPK--GACSLDGS--IYYNQEIKIMDITELGVPGSHNVENALAAISVAKLYGISNEAIK 308

Query: 298 GALKAFSGLAHRQCQVVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGK 357
      AL F G+ HR Q+V E QG +Y+DSKATN+   D +LVL+AGG +
Sbjct: 309 NALHHFHGVPVHRTQYVGEFQGRKFYNDKATNILATKMALSGFQLD---QLVLIAGGLDR 365

Query: 358 GADFHDLEPVARFCRAVVLLGRDAGLIAQALGNA-VPLVRVA-TLDEAVRQAAELAREG 415
      G F +L P + +A++ G   + A A +P+++ A + AV A EL+ EG
Sbjct: 366 GNSFDEL-IPALKGICALITFGETQNRLEDAGKKAGIPVIKTAENAEAAVPIALELSEEG 424

Query: 416 DAVLLSPACASLDMFKNFEERGRLLFAKAVEEL 447
      D++LLSPA AS D + NFE RG F +AV +L
Sbjct: 425 DSILLSPANASWDQYPNFEIRGERFMEAVNKL 456

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sp 006222      UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC      486
MURD_MYCTU 6.3.2.9) AA
      (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
      (D-glutamic acid adding enzyme) [MURD] [Mycobacterium
      tuberculosis]

```


sp O68388 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 452**
MURD_STRPY 6.3.2.9) **AA**
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) **align**
(D-glutamic acid adding enzyme) [MURD] [Streptococcus
pyogenes, Streptococcus pyogenes (serotype M3)]

Score = 175 bits (443), Expect = 2e-42
 Identities = 132/441 (29%), Positives = 214/441 (47%), Gaps = 23/441 (5%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTR---ENPPELATLRAQYPQVEVRCGELDAEFL 67
 +++GL KSG + + L + G V D++ +NP A L ++V CG E L
 Sbjct: 13 LILGLAKSGEAAAKLLTKLGALVTVNDKPFQNPAAQALLEEG---IKVICGSHPVELL 69

Query: 68 CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
 E V +PG+ P + +A AK + I +++L ++API+ ITGSN K+T TT+
 Sbjct: 70 DEDFEYMKVKNPGIPYDNPMVKRALAKEIPILTEVELAYFVSEAPIIGITGSNGKTTTTTMM 129

Query: 127 VGEMAVAADKRVAVGNGLTGTPALDLLADDI--ELYVLELSSFQLETCDRLNAEVATVLNV 184
 + ++ A + + GN+G PA ++ I + V+ELSSFQL + +A + N+
 Sbjct: 130 IADVLNAGGQSALLSGNIGYPASKVVQKAIAGDTLVMELSSFQLVGVNAFRPHIAVITNL 189

Query: 185 SEDHMDRYDGMADYHLAKHRI---FRGARQVVVNADALTRPLIADT-VPCWSFGLNKP 240
 H+D + DY AK I + +++N ++ L T F K
 Sbjct: 190 MPTHLDYHGSFEDYVAAKWMIIQAQMTESDYILILNANQEISATLAKTTKATVIPFSTQK-- 247

Query: 241 FKAFLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
 G +DG L F+ ++ +L + G+HN N G+ D + L
 Sbjct: 248 -VVDGAYLKDG--ILYFKEQAIIAATDLGVPGSHNIENALATIAVAKLSGIADDIIAQCL 304

Query: 301 KAFSGLAHRQCQVVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
 F G+ HR Q V + + +++Y+DSK+TN+ + +L+L+AGG +G +
 Sbjct: 305 SHFGGVKHLRQVRGQIKDITFYNDKSTNILATQKALSGFD---NSRLILIAGGLDRGNE 361

Query: 361 FHDLEPVARFCRAVVLLGRDAGLIAQALGNA-VPLVRVATLDEAVRQAAELAREGDAVL 419
 F DL P + +++LG A + +A A V + + EA A +LA+ GD +L
 Sbjct: 362 FDDL-VPDLLGLKQMIILGESAEARMKRAANKAEVSYLEARNVAEATELAFKLAQTGDTIL 420

Query: 420 LSPACASLDMFKNFEERGRLF 440
 LSPA AS DM+ NFE RG F
 Sbjct: 421 LSPANASWDMYPNFEVRGDEF 441

tr Q879A1 **Putative UDP-N-acetylmuramoylalanine-D-glutamate [SPS0686] 452 AA**
[Streptococcus pyogenes (serotype M3)] **align**

Score = 175 bits (443), Expect = 2e-42
 Identities = 132/441 (29%), Positives = 214/441 (47%), Gaps = 23/441 (5%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTR---ENPPELATLRAQYPQVEVRCGELDAEFL 67
 +++GL KSG + + L + G V D++ +NP A L ++V CG E L
 Sbjct: 13 LILGLAKSGEAAAKLLTKLGALVTVNDKPFQNPAAQALLEEG---IKVICGSHPVELL 69

Query: 68 CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
 E V +PG+ P + +A AK + I +++L ++API+ ITGSN K+T TT+
 Sbjct: 70 DEDFEYMKVKNPGIPYDNPMVKRALAKEIPILTEVELAYFVSEAPIIGITGSNGKTTTTTMM 129

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Sbjct: 70 DEDFEYMVKNPGIPYDNPMVKRALAKEIPILTEVELAYFVSEAPIIGITGSNGKTTTTTM 129

Query: 127 VGEMAVAADKRVAVGGNLGTPLDLLADDI--ELYVLELSSSFQLETCDRNLNAEVATVLNV 184
      + ++ A + + GN+G PA ++ I + V+ELSSFQL + +A + N+
Sbjct: 130 IADVLNAGGQSALLSGNIGYPASKVVQKAIAGDTLVMELSSFQLVGVNAFRPHIAVITNL 189

Query: 185 SEDHMDRYDGMADYHLAKHRI---FRGARQVVVNRADALTRPLIADT-VPCWSFGLNKP 240
      H+D + DY AK I + +++N ++ L T F K
Sbjct: 190 MPTHLDYHGFSFEDYVAAKWMIIQAQMTESDYILILNANQEISATLAKTTQATVIPFSTQK-- 247

Query: 241 FKAFLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
      G +DG L F+ ++ +L + G+HN N G+ D + L
Sbjct: 248 -VVDGAYLKDG--ILYFKEQAIIAATDLGVPGSHNIENALATIAVAKLSGIADDIIAQCL 304

Query: 301 KAFSGLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
      F G+ HR Q V + + +++Y+DSK+TN+ + +L+L+AGG +G +
Sbjct: 305 SHFGGVKHLRQVRGQIKDITFYNSKSTNILATQKALSGFD--NSRLILIAGGLDRGNE 361

Query: 361 FHDLEPVARFCRAVLLGRDAGLIAQALGNA-VPLVRVATLDEAVRQAAELAREGDAVL 419
      F DL P + +++LG A + +A A V + + EA A +LA+ GD +L
Sbjct: 362 FDDL-VPDLLGLKQMIILGESAERMKRAANKAEVSYLEARNVAEATELAFKLAQTGDTIL 420

Query: 420 LSPACASLDMFKNFEERGRLF 440
      LSPA AS DM+ NFE RG F
Sbjct: 421 LSPANASWDMYPNFEVRGDEF 441

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sp Q8P063 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 452
MURD_STRP8 6.3.2.9) AA
      (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
      (D-glutamic acid adding enzyme) [MURD] [Streptococcus
      pyogenes (serotype M18)]

```

Score = 174 bits (442), Expect = 2e-42
 Identities = 132/441 (29%), Positives = 213/441 (47%), Gaps = 23/441 (5%)

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Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTR---ENPPELATLRAQYPQVEVRCGELDAEFL 67
      +++GL KSG + + L + G V D++ +NP A L ++V CG E L
Sbjct: 13 LILGLAKSGEAAAKLLTKLGALVTVNDKSPFDQNPAAQALLEEG---IKVICGSHPEVELL 69

Query: 68 CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
      E V +PG+ P + +A AK + I +++L ++API+ ITGSN K+T TT+
Sbjct: 70 DENFEYMVKNPGIPYDNPMVKRALAKEIPILTEVELAYFVSEAPIIGITGSNGKTTTTTM 129

Query: 127 VGEMAVAADKRVAVGGNLGTPLDLLADDI--ELYVLELSSSFQLETCDRNLNAEVATVLNV 184
      + ++ A + + GN+G PA ++ I + V+ELSSFQL + +A + N+
Sbjct: 130 IADVLNAGGQSALLSGNIGYPASKVVQKAIAGDTLVMELSSFQLVGVNAFRPHIAVITNL 189

Query: 185 SEDHMDRYDGMADYHLAKHRI---FRGARQVVVNRADALTRPLIADT-VPCWSFGLNKP 240
      H+D + DY AK I + +++N ++ L T F K
Sbjct: 190 MPTHLDYHGFSFEDYVAAKWMIIQAQMTESDYILILNANQEISATLAKTTKATVIPFSTQK-- 247

Query: 241 FKAFLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
      G DG L F+ ++ +L + G+HN N G+ D + L
Sbjct: 248 -VVDGAYLNDG--ILYFKEQAIIAATDLGVPGSHNIENALATIAVAKLSGIADDIIAQCL 304

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Query: 301 KAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
 F G+ HR Q V + + +++Y+DSK+TN+ + +L+L+AGG +G +
 Sbjct: 305 SHFGGVKHLRQVRGQIKDITFYNDKSTNIIATQKALSGFD---NSRLILIAGGLDRGNE 361

Query: 361 FHDLREPVARFCRAVVLLGRDAGLIAQALGNA-VPLVRVATLDEAVRQAAELAREGDAVL 419
 F DL P + +++LG A + +A A V + + EA A +LA+ GD +L
 Sbjct: 362 FDDL-VPDLLGLKQMIILGESAEARMKRAANKAEVSYLEARNVAEATELAFKLAQTGDTIL 420

Query: 420 LSPACASLDMFKNFEERGRLF 440
 LSPA AS DM+ NFE RG F
 Sbjct: 421 LSPANASWDMYPNFEVRGDEF 441

sp Q8XHM4 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 458
 MURD_CLOPE 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Clostridium
 perfringens]

Score = 174 bits (442), Expect = 2e-42
 Identities = 131/453 (28%), Positives = 221/453 (47%), Gaps = 30/453 (6%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYP----QVEVRCGELDAEFL 67
 VVG+G S + L+++L + G D + + EL + ++ +E+ G LD L
 Sbjct: 19 VVGIGVSNIIPLIKFLVKLGAKVTAFTDMK-SAEELGEISKEFEILGVNLELKGKYLDR--L 75

Query: 68 CSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLV 127
 ++ +P + + + AL++ +G I+ +++ F R K + +TGS+ K+T TT+V
 Sbjct: 76 TGFEVVFKTSPMRIDSEALLRCKKQGAYITSEMEEFVRYCKGRVYGVGTGSDGKTTTTTIV 135

Query: 128 GEMAVAADKRVAVGGNLGTPALDILLAD--DIELYVLELSSSFQLETCDRLNAEVATVLNVS 185
 ++ + GGN+GTP + + + + VLELSSFQL T D + +VA V N++
 Sbjct: 136 SKLLSQEGYKTTWTGGNIGTPLFSNIEEIKEEDKVVLELSSFQLMTMD-VEIDVAIVTNIT 194

Query: 186 EDHMDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADTV-PCWSFGLNKPDPF 241
 +H+D + M +Y AK +F+ R+ +V+N + +T+ L + F K +
 Sbjct: 195 PNHLDMHKDMQEYIDAKKNVFKYQRENDLLVINDENEITKNLDKEAKGKVVRFSSKKTEG 254

Query: 242 KAFGLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALK 301
 + +DG+ ++ + ++ + I+G HN N + + ++M +
 Sbjct: 255 E--DAYYKDGLYVHGK--EVCKKDNIIKGMHNVENYLAFLAVYDE-VSIESMCKKVAE 309

Query: 302 AFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADF 361
 F G+ HRC+++RE GV YY+DS A+ + ++LLAGG K F
 Sbjct: 310 TFGGVHHRCEFIREVDGVKYNDSTASTPTRLAAGLKA----FEKPVILLAGGYDKHVPF 365

Query: 362 HDLREPVARFCRAVVLLGRDAGLIAQAL-----GNAVPLVRVATLDEAVRQAAELARE 414
 L +A+VL G I A G VP+ +L+E V A +A
 Sbjct: 366 EPLAYEGYEKIKAIIVLFVGTKEKIKAAFKRLEEEKGIHVPVYSGESLEEVVNIKSIKIAES 425

Query: 415 GDAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
 GD + LSPACAS DMFKNFE RG F + V +
 Sbjct: 426 GDIITLSPACASFDMFKNFEVRGDKFKEIVNNI 458

tr Q899G5 **UDP-N-acetylmuramoylalanine-d-glutamate ligase (EC 6.3.2.9)** 464 AA
[CTC00213] [Clostridium tetani]

align

Score = 174 bits (441), Expect = 3e-42

Identities = 136/450 (30%), Positives = 213/450 (47%), Gaps = 24/450 (5%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTR-ENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
++GLG S M LV +L+ G D + EN E + V GE + L +
Sbjct: 25 IIIGLGISNMPLVEFLSNLGRVGTGFDKKNENELENNINELKAKGVNFELGENYLDKLSNF 84

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
++ +P + P L++A ++G I+ +++ F + A + ITGS+ K+T TTL+ +
Sbjct: 85 DVVVRTPSMRTDHPILIKAKSEGAYITSEMEEFIKYCPAKLFCITGSDGKTTTTTLYNI 144

Query: 131 AVAADKRVAVGGNLGTPLDLLAD--DIELYVLELSSFQLETCDRLNAEVATVLNVSEDH 188
V VGGN+G P + + + VLELSSFQL + EVA V NVS +H
Sbjct: 145 LKTEGYTVWVGGNIGNPLFTKIEIKKDDKVLELSSFQLMSIKE-PIEVALVTNVSPNH 203

Query: 189 MDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADTVP-CWSFGLNKPDFKAF 244
+D + M +Y AK IF+ R+ +V+N + +T+ + + F + + +
Sbjct: 204 LDIHKMEEYIKAKKNIFKYQRENDLLVINEDNKITKSMEEECRGRLLKFSMKEKLKEGS 263

Query: 245 GLIEEDGQKWLAFFQDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFS 304
ED L K+ V E+K++G HN N + D+M K F+
Sbjct: 264 FYYNED----LYINEKKVCNVSEVKLGKMHNVENLLAAFSCV-SEDSSIDSMREVAKNFN 318

Query: 305 GLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDL 364
G+ HR ++V+E Q V Y++DS A++ D ++L+AGG K F L
Sbjct: 319 GVEHRLEFVKEIQEVKYFNDSIASSPTRTLAALQS---FDRPVILIAGGYDKKISFEVL 374

Query: 365 REPVARFCRAVLLGRDAGLIAQALGNAV-----PLVRVATLDEAVRQAAELAREGDA 417
+ + ++LLG I +A + P+ +++EA+ A E GD
Sbjct: 375 AKEGISHIKHLILLGDTKYKIEEAFKKVMRDSSEDLPIISICNSIEEAINIAKENGESGDV 434

Query: 418 VLLSPACASLDMFKNFEERGRLFAKAVEEL 447
V LSPACAS DMFKNFEERG F + L
Sbjct: 435 VTLSPACASFDMFKNFEERGKFKSIIRNL 464

tr Q7VEP7 **UDP-N-acetylmuramoylalanine-D-glutamate ligase MurD (EC 486
6.3.2.9)** AA
[MURD] [Mycobacterium bovis] align

Score = 174 bits (440), Expect = 3e-42

Identities = 136/417 (32%), Positives = 189/417 (44%), Gaps = 56/417 (13%)

Query: 76 SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPI-----VAITGSNAKSTVTTLVG 128
SPG S TP L AAA GV I GD++L R A + +TG+N K+T T+++
Sbjct: 73 SPGFSPATPLLAAGVPIWGDVELAWRLDAAGCYGPPRSWLVTGTNGKTTTTSMHL 132

Query: 129 EMAVAADKRVAVGGNLGTPLDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDH 188
M +A +R + GN+G+ LD+L + EL +ELSSFQL L E VLN++EDH
Sbjct: 133 AMLIAGGRRVLCGNIGSAVLVDLDEPAELLAVELSSFQLHWAPSLRPEAGAVLNIAEDH 192

Query: 189 MDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCW---SFGLNKPDKAFG 245
+D + MA+Y AK R+ G V V D + D P F L +P G

Sbjct: 193 LDWHATMAEYTAAKARVLTGG--VAVAGLDDSRAAALLDGSPAQVRVGFRLGEPAAAGELG 250

Query: 246 LIEEDGQKWLAQFD-KLLPVGELKIRGAHNYSNXXXXXXXXGHAVGLPFDAMLGALKAFS 304
 + + AF D LLPV + + G + +VG+P A+ A+ +F

Sbjct: 251 -VRDAHLVDRAFSDDLTLLPVASIPVPGPVGVLDALAAAALARSVGVPAIAIADAVTSFR 309

Query: 305 GLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDL 364
 HR + V G++Y DDSKATN ++V +AGG KGA H

Sbjct: 310 VGRHRAEVVAVADGITYVDDSKATNPHAARASVLAY-----PRVWVIAGGLLKASLHAE 364

Query: 365 REPVARFCRAVVLLGRDAGLIAQALGN---AVPLVRV----- 398
 +A VL+GRD +A+AL VP+V+V

Sbjct: 365 VAAMASRLVGAVLIGRDRAAVAEALSRHAPDVPVQVQVAGEDTGMPATVEVPVACVLDVA 424

Query: 399 -----ATLDEAVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLLFAKAV 444
 A + AV A +A+ GD VLL+PA AS D F + +RG FA AV

Sbjct: 425 KDDKAGETVGAAMTAATAVAAARRMAQPGDVTLLAPAGASFDQFTGYADRGEAFATAV 481

sp 067852 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 415
 MURD_AQUAE 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Aquifex
 aeolicus]

Score = 173 bits (439), Expect = 4e-42

Identities = 128/439 (29%), Positives = 205/439 (46%), Gaps = 37/439 (8%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V GLG+SG ++ L RG D +NP EL E L

Sbjct: 4 LVWGLGRSGKGALKLLKERGFVEYAGDSSQNP-----ELWREVLGEV 45

Query: 71 RELYVSPGLSLRTPALVQAAAGVIRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
 + +SPG+ P +A K + G+++L R K ++AITG++ KST T L +

Sbjct: 46 DTVVLSPGIPPSHPLWKEALKKEKEVVEGELELAYRFFKGKVIAITGTDGKSTTTRLTYLI 105

Query: 131 AVAADKRVAVGGNLGTPALDLLADDIE-LYVLELSSFQLETCDRLNAEVATVLNVSEDHM 189
 V GN+G P +++ ++ E + VLE+SSFQ +T + ++ S DH+

Sbjct: 106 LKKFFDEVFEGNIGKPFSEVVLENPEGIAVLEVSSFQGKTLKTRPNIGAFISFSVDHL 165

Query: 190 DRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPDKAFGLIEE 249
 D + + DY +K+RIF + D L ++ D V + + K +A ++

Sbjct: 166 DWHPSEDYLSKYRIFENQTE-----EDFL---ILNDLV---YEIKKTPSRARKVLFS 213

Query: 250 D---GQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXGHAVGLPFDAMLGALKAFSGL 306
 + + ++ +L LKIRG HN N +GL + + F GL

Sbjct: 214 ELYINSDSVFYKDIRLFNPKNLKIRGLHNVYNASVASLIALTLGLKPEDFEEVIYEFRGL 273

Query: 307 AHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLRE 366
 HR +++ GV Y+DSK+T D ++L+ GG KGADF+ LR

Sbjct: 274 PHRLEFLGNFNGVEVYNDKSTTPHALMHALKTFP---DNSVILIVGGKDKGADFYSRLH 330

Query: 367 PVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACAS 426
 V + + + +G I + + + TL+EAV+ A E+++ G+ VL SPAC+S

Sbjct: 331 IVQKKVKIALAIGETKEKIKDSWKDITEVKTCTNLEEAVKLAREVSKLGNVVLFSFACSS 390

Query: 427 LDMFKNFEERGRLFAKAVE 445
 DMF+N+EERG F + VE
 Sbjct: 391 FDMFRNYEERGEKFKELVE 409

sp O07108 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 456
 MURD_ENTFA 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Enterococcus
 faecalis (Streptococcus faecalis)]

Score = 173 bits (438), Expect = 6e-42
 Identities = 142/457 (31%), Positives = 222/457 (48%), Gaps = 38/457 (8%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRE---NPP--ELATLRAQYPQVEVRCGELDAE 65
 +V+GL KSG+S + L G V D ++ NP +L TL + V G E
 Sbjct: 13 LVLGLAKSGVSAAKLLHEL GALVTVND AKQFDQNPDAQDLLTLG-----IRVVTGGHP IE 67

Query: 66 FLCSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITG SNAKSTVT 124
 L EL V +PG+ P + +A + + I +++L + A+ PIV ITG+N K+T T
 Sbjct: 68 LLDEEFELIVKNPGIPYTNPLVAEALTRKIP IITEVELAGQIAECPIVGITGTNGKTTT 127

Query: 125 TLVGEMAVAADKRVA---VGGNLGTPALDLLADDI--ELYVLELSSSFQLETCDRLNAEVA 179
 T++G + + AD+ + GN+G PA + + + V+ELSSSFQL + + ++A
 Sbjct: 128 TMIG-LLL NADRTAGEARL AGNIGFPASTVAQEATAKDNLVME LSSFQLMGIET FHPQIA 186

Query: 180 TVLNVSEDHMDRYDGMADYHLAKHRIFRGARQ---VVVN----RADALTRPLIADTVPCW 232
 + N+ E H+D + +Y AK I + +++N L + A+ +P
 Sbjct: 187 VITNIFEAHLDYHGSRKEYVAAKWAIQNM TAEDTLILNWNQVELQTLAKTTAANVLP-- 244

Query: 233 SFGLNKPDKFAFGLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLP 292
 F + A+ L DG+ L F + ++P EL I G+HN N +
 Sbjct: 245 -FSTKEAVEGAYLL---DGK--LYFN EYIMPAD ELGIPGSHNIENALAAICVAKLKNVS 298

Query: 293 FDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXIDGKLVLLA 352
 + L FSG+ HR Q+V E Q +Y+DSKATN+ KL+LLA
 Sbjct: 299 NAQIRQTLTNFSGVPHRTQFVGEVQQR RFYND SKATNILATEMALSGFDNQ---KLLLLA 355

Query: 353 GGDGKGADFHD LREPVARFCRAVLLGRDAGLIAQAL--GNAVPLVRVATLDEAVRQAAE 410
 GG +G F +L P +A+VL G +A+A N ++ + AV A +
 Sbjct: 356 GGLDRGNSFDEL-VPALLGLKAIVLFGETKEKLAEAAKKAN IETILFAENVQTAVTIAFD 414

Query: 411 LAREGDAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
 + + D +LLSPACAS D + NFE RG F +AV++L
 Sbjct: 415 YSEKDDTILLSPACASWDQYPNFEVRGEAFMQAVQQL 451

tr Q7MWM5 UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD] 450 AA
 [Porphyromonas gingivalis (Bacteroides gingivalis)] align

Score = 173 bits (438), Expect = 6e-42
 Identities = 137/451 (30%), Positives = 208/451 (45%), Gaps = 23/451 (5%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V+G G+SG+ +GL V D + P+ +Y + G + A

Sbjct: 9 VVLGAGESGVGAALLAQAKGLHVFVSDYGKIAPKYKEELNRYA-IPYEGRHTEAIIIEA 67

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
+E+ SPG+ P + QA AK + I +I+ R A +V ITGSN K+T T +

Sbjct: 68 KEIIKSPGIPDTAPIIRQAVAKEIGIVSEIEFAGRYTDAFMVCITGSNGKTTTTMWLYHT 127

Query: 131 AVAADKRVAVGGNLG-TPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDHM 189
A V + GN+G + A + D YV+ELSSFQL+ A VA +LN++ DH+

Sbjct: 128 LCKAGLDVGLAGNVGFSLARQVAYDPPHYVIELSSFQLDNMYDFRANVAILLNITPDHL 187

Query: 190 DRYDGMAD-YHLAKHRIFRGARQ---VVVNRADALTRPLIADTVPC---WSFGLNKPDPFK 242
DRYD + Y AK RI R + + D +A+ P F +

Sbjct: 188 DRYDHRFELYAEAKMRITRNQQPEDCFIYWEDDPFISRWVAEHPPVARLLPFAMEARTDN 247

Query: 243 AFGLIEEDGQKWLAAAAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAML 297
I E + + F D+ L L + G HN N A+ + +A+

Sbjct: 248 TTAWINEKNELVVMNLNSPFVMDDEL----LALSGMHNHRNAMATAIAAKAMDIKNEAIR 303

Query: 298 GALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGK 357
AL+ F + HR + + +GV Y +DSKATNV +++L+ GG K

Sbjct: 304 EALQDFKNVPHRLEKIARVKGVDYINDSKATNVNSTWYALESMKT----RVILILGGTDTK 359

Query: 358 GADFHDLPVARFCRAVLLGRDAGLIAQALGNAVPLVRVA-TLDEAVRQAAELAREGD 416
G D+ D+ V ++ LG D + + + + A ++ EAV A ++A +GD

Sbjct: 360 GNDYTDIENLVLSKVDGLIFLGIDNEKLHKFFDGKISRADACSMHEAVSLAYKMASKGD 419

Query: 417 AVLLSPACASLDMFKNFEERGRLEFAKAVEEL 447
VLLSPACAS D+F+N+E+RG F K V L

Sbjct: 420 TVLLSPACASFDLFQNYEDRGDQFRKEVLNL 450

tr Q89FU5 **UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD]** 466 AA
[Bradyrhizobium japonicum] align

Score = 169 bits (428), Expect = 8e-41

Identities = 151/462 (32%), Positives = 211/462 (44%), Gaps = 42/462 (9%)

Query: 12 VVGLGKSGMSLVRYLARRGLP-FAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
V GLG SG++ L G A D EN + A +A+ ++R D + A

Sbjct: 14 VFGLGGSGLASCHALKAGGAEVIAADDNAENVAKAA--QAGFITADLR----DVSWAGFA 67

Query: 71 RELYVSPGLSLRTP----ALVQAAAKGVRISGDIDLFAREAK----APIVAITGSNAKS 121
L ++PG+ L P ++++A GV + GDI+LF RE + AP VAITG+N KS

Sbjct: 68 A-LVLAPGVPLTHPVPHWSVLKAREAGVEVIGDIELFCRERRRRHAPDAPFVAITGTNGKS 126

Query: 122 TVTTLVGEMAVAADKRVAVGGNLGTALDLLADDI-ELYVLELSSFQLETCDRLNAEVAT 180
T T L+ + A +GGN+GT L L ++V+E+SS+Q++ L+ V

Sbjct: 127 TTTALIAHLTKVAGYDTQMGGNIGTAILSLEPPRTGRVHVIESSYQIDLTPSLDPSVGI 186

Query: 181 VLNVSEDHMDRYDGMADYHLAKHRIFRGARQ---VVVNRADALTRPLIADTVPCWSFGLN 237
+LNVSEDH+DR+ +A Y K R+ G + +V D R IAD + +

Sbjct: 187 LLNVSEDHIDRHGTIAHYAAVKERLVAGVQAGGTSIVGVDDGYCRD-IADRLDRAGKNVV 245

Query: 238 KPDPFK---AFGLIEEDGQ-----KWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAV 289
+ K A G+ E G + KL +G L RG HN N A+

Sbjct: 246 RISVKNPLASGIHVEHGTIVRTAGGARSEVAKLGGIGSL--RGLHNAQNAACAAAALAM 303

Query: 290 GLPFDAMLGALKAFSGLAHRQCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLV 349
 G+ D + L++F GLAHR + V R V + +DSK TN +
 Sbjct: 304 GISQDVLQDGLRSFPGLAHRMEQVGRGNVLFVNDKGTNADATAHALSSF-----ADIF 358

Query: 350 LLAGGDGKGFHDLREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAA 409
 +AGG K L R R L+G A + LG V TLD AV AA
 Sbjct: 359 WIAGGKPKAGGITSLTGFFPRI-RKAYLIGEAAQEFSGTLGTQVAHEISQTLDDVAVEHAA 417

Query: 410 ELAREGD---AVLLSPACASLDMFKNFEERGRLEFAKAVEEL 447
 A VLLSPACAS D ++NFE RG F + V+ L
 Sbjct: 418 RDAEASGLTDAVVLLSPACASFDQYRNFEIRGTFKRELQAL 459

sp Q8CSX6 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 449
 MURD_STAEF 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)
 (D-glutamic acid adding enzyme) [MURD] [Staphylococcus align
 epidermidis]

Score = 168 bits (426), Expect = 1e-40
 Identities = 120/435 (27%), Positives = 211/435 (47%), Gaps = 14/435 (3%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +VVGL KSG + L + G V D ++ + + +EV G L
 Sbjct: 13 LVVGLAKSGYEAAKLLLKLGANVKVNDGKDLSQDAHAKDLESMGIEVISGSHPFSLDDDD 72

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
 + +PG+ + +A +G++I +++L ++API+A+TG+N K+TVT+L+G+M
 Sbjct: 73 PIIVKNPGIPYTVSIIKEATNRGLKILTEVELSYLISEAPIIAVTGTNGKTTVTSLIGDM 132

Query: 131 AVAADKRVAVGGNLGTPLDALLAD--DIELVLELSSFQLETCDRLNAEVATVLNVSEDH 188
 + + GN+G A + + E + ELSSFQL + +A + N+ H
 Sbjct: 133 FQKSVLTGRLSGNIGYVASKVAQEVKSDEYLITELSSFQLLGIEEYKPHIAIITNIYSAH 192

Query: 189 MDRYDGMADYHLAKHRIFRGARQVVVNRA DALTRPLI-ADTVPCWSFGLNKPDKFAFGLI 247
 +D ++ + +Y AK +I++ + + R LI ++ + +F + + G+
 Sbjct: 193 LDYHETLENYQNAKKQIYKNQTKDDYLYCNHQRHLIESENLEAKTFYFSTQQ-EVDGIY 251

Query: 248 EEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLA 307
 +DG ++ F +++ +L + G HN N G+P A++ +L FSG+
 Sbjct: 252 IKDG--FIVFNGIRIINTKDLVLPGEHNLENILAAVLASIIAGVPVKAIVDSLVTFSGID 309

Query: 308 HRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGFHDLREP 367
 HR Q++ + YY+DSKATN D ++ L GG +G +F +L P
 Sbjct: 310 HRLQYIGTNRTNKKYNDKATN----TLATQFALNSFDQPIIWLCGGLDRGNEFDEL-IP 364

Query: 368 VARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDAVLLSPACA 425
 R +V+ G A+ LGN+ +++ +++AV + ++ D VLLSPACA
 Sbjct: 365 YMENVVRVMVVFGETQDKFAK-LGNSQGYVIKATDVEDAVDKIQDIVEPNDVVLLSPACA 423

Query: 426 SLDMFKNFEERGRLEF 440
 S D + FEERG F
 Sbjct: 424 SWDQYHTFEERGEKF 438

sp Q52953 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 463
MURD_RHIME 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Rhizobium
meliloti (Sinorhizobium meliloti)]

Score = 168 bits (425), Expect = 2e-40
Identities = 145/456 (31%), Positives = 209/456 (45%), Gaps = 37/456 (8%)

Query: 14 GLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSAREL 73
GLG SG++ + L G D +NP +A A + +L +
Sbjct: 16 GLGGSLATAQALVSGGADVVAWD--DNPDSVAKAAA---AGIATADLRGADWHAFAAF 69

Query: 74 YVSPGLSLRTP----ALVQAAAKGVRISGDIDLFAREAK-----APIVAITGSNAKSTVT 124
+SPG+ L P ++ A GV I GD++LF RE + P +AITG+N KST T
Sbjct: 70 VLSPGVPLTHPKPHWSVDLAHQAGVEIIGDVELFVRERRKHAPDCPFIAITGTNGKSTTT 129

Query: 125 TLVGEMAVAADKRVAVGGNLTGPALDLLADDI-ELYVLELSSFQLETCDRLNAEVATVLN 183
L+ + + + +GGN+GT L L YV+E SS+Q++ L+ +LN
Sbjct: 130 ALIAHILRTSGRDTQLGGNIGTAVLTLDPPKAGRFYVVECSSYQIDLAPTLDPAGILLN 189

Query: 184 VSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVP--CWSFGLNKP 240
++ DH+DR+ M Y K R+ G+ VV D+L+ LIAD V +++
Sbjct: 190 LTPDHLDRHGTMQHYADIKERLVAGSGTAVVGVDLSLS-SLIADRVERAGTKVVRISRRH 248

Query: 241 FKAFLIEED-----GQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDA 295
A G+ E Q + F L G +RG HN N AVG+
Sbjct: 249 PLAEGIYAEGSALMRAQDGASSLFTDL--AGIQTLRGGHNAQNAAAAIAACLAVGISGKD 306

Query: 296 MLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGD 355
++ L++F GL HR Q V ++ V + +DSKATN ++ +AGG
Sbjct: 307 IVDGLRSFPGLKHRMQPVAKKGEVVFVNDKATNAEAAAPALSSY-----DRIYWIAGGL 361

Query: 356 GKGADFHDRLREPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDEAV-RQAAELARE 414
K L + +A L+G A A LG AVP TL++AV AA+ AR+
Sbjct: 362 PKEGGITSLAPFFPKIVKA-YLIGEAAAPSFAATLGEAVPYEISGTLEKAVAHAAADAARD 420

Query: 415 GD---AVLLSPACASLDMFKNFEERGRLFAKAVEEL 447
AV+LSPACAS D +KNFE RG F V L
Sbjct: 421 SQGPAAVMLSPACASFDQYKNFEVRGDAFVGHVAAL 456

sp O33595 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 449
MURD_STAAM 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Staphylococcus
aureus (strain Mu50 / ATCC 700699), Staphylococcus
aureus (strain N315), Staphylococcus aureus]

Score = 167 bits (423), Expect = 3e-40
Identities = 117/434 (26%), Positives = 209/434 (47%), Gaps = 12/434 (2%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+VVGL KSG + L++ G V D ++ + + V G L +
Sbjct: 13 LVVGLAKSGYEAAKLLSKLGANVTVDNGKDLSDAHAKDLESMGISVVGSHPLTLLDNN 72

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130

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      + +PG+      + +A +G++I +++L ++API+A+TG+N K+TVT+L+G+M
Sbjct: 73  PIIVKNPGIPYTVSIIDEAVKRGLKILTEVELSYLISEAPIIAVTGTNGKTTVTSLIGDM 132

Query: 131 AVAADKRVAVGGNLGTPLDLLAD--DIELYVLELSSSQLETCDRLNAEVATVLNVSEDH 188
      +      + GN+G A + + + V ELSSSQQL ++ +A + N+ H
Sbjct: 133 FKKSRLTGRLSGNIGYVASKVAQEVKPTDYLVTLELSSSQQLLGIEKYKPHIAIITNIYSAH 192

Query: 189 MDRYDGMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDKAFGLIE 248
      +D ++ + +Y AK +I++ + + R +I + G+
Sbjct: 193 LDYHENLENYQNAKKQIYKNQTEEDYLCNYHQEQVIESEELKAKTLYFSTQQEVDGIYI 252

Query: 249 EDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAH 308
      +DG ++ ++ +++ +L + G HN N G+P A++ +L FSG+ H
Sbjct: 253 KDG--FIVYKGVRIINTEDLVLPGEHNLENILAAVLACILAGVPIKAIIDSLLTTFSGIEH 310

Query: 309 RCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPV 368
      R Q+V + YY+DSKATN + ++ L GG +G +F +L P
Sbjct: 311 RLQYVGTNRNTNKYYNSKATN----TLATQFALNSFNQPIIWLCGGLDRGNEFDEL-IPY 365

Query: 369 ARFCRAVLLGRDAGLIAQALGNA--VPLVRVATLDEAVRQAELAREGDAVLLSPACAS 426
      RA+V+ G+ A+ LGN+ ++ +++AV + ++ D VLLSPACAS
Sbjct: 366 MENVRAMVVFVGQTKAKFAK-LGNSQGKSVIEANNVEDAVDKVQDIIEPNQDVLLSPACAS 424

Query: 427 LDMFKNFEERGRLF 440
      D + FEERG F
Sbjct: 425 WDQYSTFEERGEKF 438

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sp Q8NX35 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 449
MURD_STAAW 6.3.2.9) AA
      (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
      (D-glutamic acid adding enzyme) [MURD] [Staphylococcus
      aureus (strain MW2)]

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Score = 167 bits (422), Expect = 4e-40

Identities = 117/434 (26%), Positives = 209/434 (47%), Gaps = 12/434 (2%)

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Query: 11  IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
      +VVGL KSG + L++ G V D ++ + + + V G L +
Sbjct: 13  LVVGLAKSGYEAAKLLSKLGANVTVNDGKDLSDAHVKDLESMGISVSVSGSHPLTLLDNN 72

Query: 71  RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
      + +PG+ + +A +G++I +++L ++API+A+TG+N K+TVT+L+G+M
Sbjct: 73  PIIVKNPGIPYTVSIIDEAVKRGLKILTEVELSYLISEAPIIAVTGTNGKTTVTSLIGDM 132

Query: 131 AVAADKRVAVGGNLGTPLDLLAD--DIELYVLELSSSQLETCDRLNAEVATVLNVSEDH 188
      +      + GN+G A + + + V ELSSSQQL ++ +A + N+ H
Sbjct: 133 FKKSRLTGRLSGNIGYVASKVAQEVKPTDYLVTLELSSSQQLLGIEKYKPHIAIITNIYSAH 192

Query: 189 MDRYDGMADYHLAKHRIFRGARQVVVNADALTRPLIADTVPCWSFGLNKPDKAFGLIE 248
      +D ++ + +Y AK +I++ + + R +I + G+
Sbjct: 193 LDYHENLENYQNAKKQIYKNQTEEDYLCNYHQEQVIESEELKAKTLYFSTQQEVDGIYI 252

Query: 249 EDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGLAH 308
      +DG ++ ++ +++ +L + G HN N G+P A++ +L FSG+ H
Sbjct: 253 KDG--FIIYKGVRIINTEDLVLPGEHNLENILAAVLACILAGVPIKAIIDSLLTTFSGIEH 310

```

Query: 309 RCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFHDLREPV 368
R Q+V + YY+DSKATN + ++ L GG +G +F +L P
Sbjct: 311 RLQYVGTNRNTRYNDKATN----TLATQFALNSFNQPIIWLCGGLDRGNEFDEL-IPY 365

Query: 369 ARFCRAVLLGRDAGLIAQALGNA--VPLVRVATLDEAVRQAAELAREGDAVLLSPACAS 426
RA+V+ G+ A+ LGN+ ++ +++AV + ++ D VLLSPACAS
Sbjct: 366 MENVRAMVVFQGTAKFAK-LGNSQGKSVIEANNVEDAVDKVQDIIEPNDVVLLSPACAS 424

Query: 427 LDMFKNFEERGRLF 440
D + FEERG F
Sbjct: 425 WDQYSTFEERGEKF 438

trnew AAS04216 MurD [MURD] [Mycobacterium paratuberculosis] 489 AA
align

Score = 166 bits (421), Expect = 5e-40
Identities = 149/478 (31%), Positives = 213/478 (44%), Gaps = 55/478 (11%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQ-VEVRCGELDAEFLCS 69
+V G G +G +++ L R G + D ++P ATLR V+ AE +
Sbjct: 18 LVAGGGITGRAVLAALRRFGAAPTLCDDDP---ATLRGYVDSGVDTVSTSAEAERISR 72

Query: 70 ARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPI-----VAITGSNAKST 122
+ SPG + P + AAA GV + GD++L R A + +TG+N K+T
Sbjct: 73 YALVVTSPGFAPTAPLPLAAAAAGVPVWGDVELAWRLDVAGHYGPPRRWLVTGTNGKTT 132

Query: 123 VTTLVGEMAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSSFQLETCDRNLNAEVATVL 182
T+++ M AA +R + GN+G+P LD+L EL +ELSSFQL L E VL
Sbjct: 133 TTSMHLAMLTAAARRSLCGNIGSPVLDVLDQPAELLAVELSSFQLHWAPSLRPEGGA VL 192

Query: 183 NVSEDHMDRYDGMADYHLAKHRIFRGARQVVNRRADALTRPLIADTVPCWSFGLNKPDPFK 242
N++EDH+D + +ADY AK R+ G R VV D+ L++ G +
Sbjct: 193 NIAEDHLDWHGTLADYAAAKARVLDG-RVAVVGLDDSRAAALLSTARAPVRVGFRLGEPA 251

Query: 243 AFGLIEEDGQKW-LAFQFD-KLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
A L GQ AF D LLPV + + G + V +P + A+
Sbjct: 252 AGELGVRGGQLVDRAFADDLTLLPVDSIPVPGVGVLDALAAALARCVDVPASPIAEAI 311

Query: 301 KAFSGLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
+F HR + V G++Y DSKATN ++V +AGG KGA
Sbjct: 312 VSFRVGRHRAEVAVADGITYVDDSKATNPAAEASVLAY-----PRVWVIAGGLLK GAS 366

Query: 361 FHDLEPVARFCRAVLLGRDAGLIAQALGN---AVPLVRVAT----- 400
+A + VL+GRD +A+AL VP+V V T
Sbjct: 367 VDAEVARMASWLVGAVLIGRDRREVAEALSRHAPDVPVHVVTGEDAGMDATPVVFGANV 426

Query: 401 -----LDEAVRQAAELAREGDAVLLSPACASLDMFKNFEERGR LFAKAV 444
+ AV A +LA+ GD VLL+PA AS D F + +RG FA AV
Sbjct: 427 TKVKHLGGDLGAAVMSAAVAAARDLAKPGDTVLLAPAGASFDQFAGYADRGEAFAAV 484

sp Q98KB1 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 466
MURD_RHILO 6.3.2.9) AA

(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Rhizobium loti
 (Mesorhizobium loti)]

Score = 164 bits (415), Expect = 3e-39

Identities = 139/455 (30%), Positives = 201/455 (43%), Gaps = 35/455 (7%)

Query: 14 GLGKSGMSLVRYLARRGLPFAVVDTRENPPPELATLRAQYPQVEVRCGELDAEFLCSAREL 73
 GLG SG++ R L G D +NP +A A + +L
 Sbjct: 16 GLGSGIATARALIEGGAQVLAWD--DNPDSVAKAAA----TGIATADLRGADWAKFSAP 69

Query: 74 YVSPGLSLRTP----ALVQAAAKGVRISGDIDLFAREA-----KAPIVAITGSNAKSTVT 124
 +SPG+ L P + A GV + GDI+LF RE AP +AITG+N KST T
 Sbjct: 70 VLSPGVPLTHPKPHWTVELAKGAGVEVIGDIEFCRERILQAPTAPFIAITGTNGKSTTT 129

Query: 125 TLVGEMAVAADKRVAVGGNLTGTPALDLLADDIEL-YVLELSSFQLETCDRLNAEVATVLN 183
 L + +A + +GGN+G + L + +V+E SS+Q++ +N +LN
 Sbjct: 130 ALTAHILKSAGRDTQMGGNIGRAVMTLDPKPKDRHFVVECSSYQIDLAPSINPTAGILLN 189

Query: 184 VSEDHMDRYDGMADYHLAKHRIFRGARQVVNRADALTRPLIADTVPCWSFGLNKPDKFA 243
 ++ DH+DR+ M Y K R+ G+ ++ D+ IA+ + + + K
 Sbjct: 190 LTPDHLDRHGTMQHYASIKERLVAGSETAIIGIDDSWCAQ-IAERLERAGQQVIRIS-KR 247

Query: 244 FGLIE---EDGQKWLAFFQFDKLLPVGELK----IRGAHNYSNXXXXXXXXXGHAVGLPFDAM 296
 L + DG + + V L+ +RG HN N VGL +
 Sbjct: 248 LPLTDGYFADGTNLMEAVHGRYSKVAFLLEGIGSLRGQHNAQNALAAVAACLKVLGLDLGEI 307

Query: 297 LGALKAFSGLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDG 356
 L++F GLAHR + V + V + +DSKATN ++ +AGG
 Sbjct: 308 QSGLESFPGLAHRMEQVGRKDHVLFVNDKATNADAAAPALSSF-----PRIYWIAGGLP 362

Query: 357 KGADFHDLEPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGD 416
 K LR R +A L+G A + LG AVP TL AV AA A + D
 Sbjct: 363 KEGGIEPLRGFFPRIAKA-YLIGEAPAFSATLGEAVPYEISGTLAAVAHAHAHDAKDD 421

Query: 417 A----VLLSPACASLDMFKNFEERGRLEFAKAVEEL 447
 + VLLSPACAS D FKNFE RG F +A +
 Sbjct: 422 SGEVVVLLSPACASFDQFKNFEVRGEAFRQAASAI 456

sp P57995 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 490
 MURD_MYCLE 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Mycobacterium
 leprae]

Score = 163 bits (413), Expect = 5e-39

Identities = 146/483 (30%), Positives = 213/483 (43%), Gaps = 58/483 (12%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V G G +G +++ L R G+ + D + P A V +
 Sbjct: 12 LVAGGGVTGRAVLAALTRFGMAATLCD---DDPAALQQYADNGVATVSAATATQQMFERG 68

Query: 71 RE---LYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPI-----VAITGSNAK 120
 R+ + SPG + TP LV A+A V I GD++L R A + +TG+N K
 Sbjct: 69 RKYVLVVTSPGFAPTPVLVAASAARVPIWGDVELAWRLDAAGYYGPPRRWLVTGTNGK 128

Query: 121 STVTTLVGEMAVAADKRVAVGGNLTGTPALDLL---ADDIELYVLELSSSFQLETCDRLNAE 177
 +T T+++ M A ++R + GN+G P LD+L A+ + +ELSSFQL L E
 Sbjct: 129 TTTTSMHLAMLAADNRRSLLCGNIGRPVLDVLTEFAEPSDFLAVELSSSFQLHWAPSLRPE 188

Query: 178 VATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLN 237
 VLN++EDH+D + MADY +AK R+ G R VV D+ L++ TV G
 Sbjct: 189 AGVVLNIAEDHLDWHSTMDYTMAKARVLTG-RVAVVGLDDSRAAALLSTTVAPVRVGFR 247

Query: 238 KPDKFAFGLIEEDGQKW-LAFQFD-KLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDA 295
 + L DG AF D L+PV + + G + +VG+ A
 Sbjct: 248 FGEPAVGELGVRDGYLVDRFAEDLALMPVTSIPVSGPVGVLDAALAAALARSVGVGATA 307

Query: 296 MLGALKAFSGLAHRCQVVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGD 355
 + A+ F HR + V G+ Y DDSKATN ++V +AGG
 Sbjct: 308 IADAVAFRLGRHRAEVVAVADGIRYVDDSKATNPHAALVSVLAYP-----RVVWVAGGL 362

Query: 356 GKGADFHDLREPVARFCRAVLLGRDAGLIAQALGNA---VPLVRVATLDEA----- 404
 KGA +A VL+GRD ++A+AL VP+V+V ++A
 Sbjct: 363 LKGASVDAEVARMAPQLVGAVLIGRDRAMVAEALSRHAPNVPVQVQVAGEDAGMHAVAVV 422

Query: 405 -----VRQAAELAREGDAVLLSPACASLDMFKNFEERGRFLFA 441
 V A +LA+ GD VLL+PA AS D F + +RG FA
 Sbjct: 423 SGTDIVISISDVGGTIGTRVMVAAVAARDLAQPGDTVLLAPAGASFDQFSGYADRGDTFA 482

Query: 442 KAV 444
 AV
 Sbjct: 483 TAV 485

sp Q8YPS9 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC** 462
 MURD_ANASP **6.3.2.9)** AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Anabaena sp.
 (strain PCC 7120)]

Score = 163 bits (413), Expect = 5e-39

Identities = 137/453 (30%), Positives = 214/453 (46%), Gaps = 24/453 (5%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRA-QYPQVEVRCGELDAEFLCSA 70
 VVGLGKSG++ R L R G + D+ + L + Q+ V G +F +
 Sbjct: 6 VVGLGKSGVAAARLLKREGWEVVLSDSNTSDTLKQQQELAKEQITVELG-YSLDFAGAL 64

Query: 71 RELY-VSPGLSLRTPALVQAAAKGVRISGDIDLFAREKA-PIVAITGSNAKSTVTTLVG 128
 +L VSPG+ P LV+A G+ G+++L R K+ P V ITG+N K+T T L+
 Sbjct: 65 PDLIIIVSPGVPWDIPDLVKARDLGIETIGEMELAWRHLKSLPWVGITGTNGKTTTTALIA 124

Query: 129 EMAVAADKRVAVGGNLTGTPALDLLADDI--ELYVLELSSSFQLETCDRLNAEVATVLNVSE 186
 + AA GN+G A ++ +I + + E+SS+Q+E+ L ++ +
 Sbjct: 125 AIFQAAGFDAPACGNIGYAAACEVALAEIPPDWIIIGEMSSYQIESSVTLAPHISIWTTFTF 184

Query: 187 DHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVP--CWSFGLNKPDKFAF 244
 DH+ R+ + +Y+ K ++ R + V N DA + A P W+ K
 Sbjct: 185 DHLARHKTLENYDDIKAKLLRQSHLQVFNGDDAYLSKIGASHWPDAYWTSVQGKESLLGE 244

Query: 245 -GLIEEDGQKWLAFFQF-----DKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLG 298
 G EDG W+ Q +++ L++ GAHN N + +A+

Sbjct: 245 KGFYIEDG--WVVEQLPNSPPQRIVEASALRMVGAHNLQNLLMAVAAARLADISPNAIDK 302

Query: 299 ALKAFSGLAHRQCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKG 358
 A++ F G+AHR + + +G+ + +DSKATN + +VL+AGG+ K

Sbjct: 303 AVREFPGVAHRLEHICTWEGIDFINDSKATN----YDAAEVGLASVKSPVVLIAAGGEAKP 358

Query: 359 ADFHDLREPVARFCRAVLLGRDAGLIAQALGNA--VPLVRVATLDEAVRQAAELAREGD 416
 D + AV+L+G A AQ L V T+++AVR++ ELA+

Sbjct: 359 GDDTAWLAKIQAQTSALLIGSAAAPAFARLKEVGYTHYEIVETMEKAVRRSLELAKHHQ 418

Query: 417 A--VLLSPACASLDMFKNFEERGRLEFAKAVEEL 447
 A VLLSPACAS D + NFE RG F + EL

Sbjct: 419 APVLLSPACASFDQYPNFEARGDHFRELCEL 451

sp Q88V80 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 459**
 MURD_LACPL 6.3.2.9) **AA**
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) **align**
 (D-glutamic acid adding enzyme) [MURD] [Lactobacillus
 plantarum]

Score = 163 bits (412), Expect = 6e-39

Identities = 133/454 (29%), Positives = 212/454 (46%), Gaps = 31/454 (6%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTR---ENPPELATLRAQYPQVEVRCGELDAEFL 67
 +V+GL KSG++ R L + G V D + ENP L ++V G L

Sbjct: 13 LVLGLAKSGVNAARLLHKLGAFTVNDKKKFDENPDQAQELLS--DGIKVITGGHPLSL 69

Query: 68 CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
 ++ V +PG+ P + A KG+ + +++L ++ ++ +TG+N K+T TT+

Sbjct: 70 DEDFKVVVKNP GIPYSNPVSGAQEKGIPVITEVELASQILAGELIGVTGTNGKTTTTT 129

Query: 127 VGEMAVAADK--RVAVGGNLGTPALDLL--ADDIELVLELSSFQLETCDRLNAEVATVL 182
 + M + V GN+G PA + A + V ELSSF L L+ +A +

Sbjct: 130 ITMMLNQRTNAGKAYVAGNIGVPASAIQAQKATAADTMVTELSSFMCGIQTLPHPHIAVIT 189

Query: 183 NVSEDHMDRYDGMADYHLAKHRIFRG--ARQVVVNRA-----LTRPLIADTVPCWSFG 235
 N+ H+D + +Y AK RI A +V D+ L++ A VP +S

Sbjct: 190 NIYSTHLDYHGSRENYVKAKMRITMNQTANDYLVINWDSEEWRLSKQSQATVVP-FSRQ 248

Query: 236 LNKPDFKAFGLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDA 295
 N D G EE G+ L F+ + ++ +++I G HN N +P

Sbjct: 249 ANTKD---GAYEEAGK--LYFKDEYIMDAADIRIPGDHNVENALAAIAVAKLQAVPTAG 302

Query: 296 MLGALKAFSGLAHRQCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGD 355
 ++ LK F+G+ HR Q+V Q +Y+DSKATN+ D ++LLAGG

Sbjct: 303 IVQVLKTFGTGVRHRTQYVETYQDRQFYNDKATNL----VSTEMALKGFDQPVILLAGGL 358

Query: 356 GKGADFDHDLREPVARFCRAVLLGRDAGLIAQA--LGNAVPLVRVATLDEAVRQAAELAR 413
 +G F L + + +++ G A +A A L + + AV A + ++

Sbjct: 359 DRGNTFEKLAPALKAHVKT LIVFGETA EK MADAGRLAGIQDIEFTDNCETAVPIAWQHSQ 418

Query: 414 EGDVLLSPACASLDMFKNFEERGRLEFAKAVEEL 447
 GD ++LSPACAS D + NFE RG F KA+E+L

Sbjct: 419 AGDIIMLSPACASWDQYPNFEVRGDRFIKAIEQL 452

trnew CAE28973 **UDP-N-acetylmuramoylalanine-D-glutamate ligase precursor** 469
 (EC AA
 6.3.2.9) [MURD] [Rhodopseudomonas palustris] align

Score = 160 bits (405), Expect = 4e-38
 Identities = 131/408 (32%), Positives = 191/408 (46%), Gaps = 46/408 (11%)

Query: 73 LYVSPGLSLRTPA----LVQAAAKGVRISGDIDLFAREAKA-----PIVAITGSNAKSTV 123
 L ++PG+ L PA +++A GV + GD++LF RE KA P VAITG+N KST
 Sbjct: 69 LVLTPGVPLTHPAPHWTVLKAQEAGVEVIGDVELFCRERKAHAPRAPFVAITGTNGKSTT 128

Query: 124 TTLVGEMAVAADKRVAVGGNLGTPALDLLAD-DIELYVLELSSFQLETCDRLNAEVATVL 182
 T L+ + A +GGN+GT L L D ++V+E+SS+Q++ L+ V +L
 Sbjct: 129 TALIAHLLREAGWDTQLGGNIGTAILSLEPPKDG RVHVIEMSSYQIDLTPLSDPTVGILL 188

Query: 183 NVSEDHMDRYDGMADYHLAKHRIFRGAR-----QVVVNRADALTRPLIADT 228
 NV+EDH+DR+ + Y K R+ G + + +R + + ++ +
 Sbjct: 189 NVTEDHIDRHGTIEHYAAVKERLVAGVQDGGTSIIGVDDEFGRAAADRIERAGKRVVRMS 248

Query: 229 VP-CWSFGLNKPDKFAFLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGH 287
 V +FG+ D + ++ +A KL +G L RG HN N
 Sbjct: 249 VQGPVTFGIT-ADLDSIRRVDDGGTSTEVA----KLGGIGSL--RGLHNAQNAAAAAAAVL 301

Query: 288 AVGLPFDAMLGALKAFSGLAHRCQWVRERQG---VSYYDDSKATNVXXXXXXXXXXXXXD 343
 A+G+ + + L++F GLAHR + V + G + +DSKATN
 Sbjct: 302 ALGVSPPEVLQQGLRSFPGLAHRMEQVGRQVGEQGTTLFVNDSKATNADAAAKALASF--- 358

Query: 344 IDGKLVLLAGGDGKGADFDHDLREPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDE 403
 G + +AGG K L E R R L+G+ A A L VP TL+
 Sbjct: 359 --GDIFWIAGGKPKTGGIESLAEIFPRI-RKAYLIGQAAQEFAATLEGRVPYEISETLEA 415

Query: 404 AV----RQAAELAREGDAVLLSPACASLDMFKNFEERGRLFKAVEEL 447
 AV R AA VLLSPACAS D F+NFE RG F + V L
 Sbjct: 416 AVPAAARDAAASGLAEPVLLSPACASFDQFRNFELRGTRFRELVTAL 463

sp Q8FNT8 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC** 475
 MURD_COREF 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Corynebacterium
 efficiens]

Score = 159 bits (401), Expect = 1e-37
 Identities = 136/455 (29%), Positives = 198/455 (42%), Gaps = 31/455 (6%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V G G SG + L GL V + E + V+V E L
 Sbjct: 21 LVTGAGVSGTGIAGMLHDLGLDVVVAEDNETSRHRLI---ELLDVDVVGTEHARASLGDY 77

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPI-----VAITGSNAKSTV 123
 + SPG +P LV AA++G+ + GD++L R +A + +A+TG+N K+T
 Sbjct: 78 SIVVTSPGWRPDSPLVDAASRGLEVIGDVELAWRLDRAGVFGVSRTWLAVTGTNGKTTT 137

Query: 124 TTLVGEMAVAADKRVAVGGNLGTPALDLLA--DDIELYVLELSSFQLETCDRLNAEVATV 181
 T ++ M GN+G P L D +++ V ELSSFQL L + V

Sbjct: 138 TAMLAAMMKQGGFNAVAVGNIGVPVSAALTSCDRVDMVAELSSFQLHWAPTLPDAGLV 197

Query: 182 LNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADT--VPCWSFGLNKP 239
LN++EDH+D + DY LAK R+ A V+ D+ L + F L +P

Sbjct: 198 LNLAEHDHIDWHGSFRDYALAKTRVLT-APVAVIGADDSYLVELTTELGLSGLIGFTLGEP 256

Query: 240 DFKAFGLIEED-GQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLG 298
+ G++ A Q L P + G + + G+ + + G

Sbjct: 257 GPRQLGVNLGHLDVNAFAAQLP-LAPADGINPSGPAGVLDALAAAVARSQGVSAEDIAG 315

Query: 299 ALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKG 358
AL F HR Q V E GV + D+SKATN ++ + GG KG

Sbjct: 316 ALATFEVSGHRGQVVAEDHGVQFIDNSKATNPAAADTALAGRES-----VIWIVGGQLKG 370

Query: 359 ADFHDLREPVARFCRAVVLLGRDAGLIAQALGNAVP--LVRV-----ATLDEAVRQAA 409
AD +L A +A ++LG D I A+ P ++RV A + E V A

Sbjct: 371 ADISELVATHARIKAALVLGADRAEIVTAVEQHAPDAMIRVTDSTDPVAMRELVDHAF 430

Query: 410 ELAREGDAVLLSPACASLDMFKNFEERGRLEFAKAV 444
A GD VLL+PA ASLDM+K +RG +FA+AV

Sbjct: 431 RFAEPGDCVLLAPAAASLDMYKGMQGRGDIFAEAV 465

tr Q7U8T1 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) 462
[MURD] AA
[Synechococcus sp. (strain WH8102)] align

Score = 157 bits (396), Expect = 4e-37

Identities = 130/464 (28%), Positives = 209/464 (45%), Gaps = 38/464 (8%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENNP--ELATLRAQYPQVEVRCGELDAEF- 66
+VVGLG+SG R L G P +V+D+ + + LR Q +V+++ F

Sbjct: 5 VVVGLGRSGQGAARLLQATGHPVSVIDSGQGEQLEKKAEGLRQQGVEVQLQAPLAIDSR 64

Query: 67 --LCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAK-APIVAITGSNAKSTV 123
L + + +SPG+ P L +GV + G++ + K P V ITG+N K+TV

Sbjct: 65 PWLDQLQRVVISPGVPWDHPTLDDLRQRGVAVDGEMAVAWDALKHIPWVGITGTNGKTTV 124

Query: 124 TTLVGEMAAADKRVAVGGNLGTPALDLLADDIELY-----VLELSSFQLETCDRLNA 176
T L+ + A +GGN+G A ++ + + + V+ELSS+Q+E R+

Sbjct: 125 THLLSHVLCQAGLAAPMGGMVSAEALNLQOEHTTAPDWLVMELSSYQIEAAKRIRP 184

Query: 177 EVATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGL 236
+ ++ DH++R+ + Y K + + + N D P + W+ G

Sbjct: 185 RIGIWTTLTPDHLEHGTVEAYRAIKRGLLERSDHAIFNADD----PDLRQQRQSWTGGT 240

Query: 237 -----NKPDKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVG 290
+PD L +G+ W+ + L P L + GAHN N +G

Sbjct: 241 WWSAESAQPDGHPADLWI-NGKGVCDRSQPLFPALAMPGAHNRQNLVLTAAARQIG 299

Query: 291 LPFDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLV 350
L +++ L++F G+ HR + V ++DSKATN + G +V+

Sbjct: 300 LSPASIVAGLRSFPGVPHRLEPVGRIGNAQVFNDKATNYDAAAVGLKA----MQGPVVV 355

Query: 351 LAGGDGKGADFDHDLREPVARFCRAVVLLGRDA---GLIAQALGNAVPLVR---VATLDE 403
LAGG K D E + R AVVL G GLI A R + ++E

Sbjct: 356 LAGGSTKQGDATGWLEELNRKACAVVLFAGASTEELHGLITGANFTGELTRRTDLTSAVEE 415

Query: 404 AVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLLFAKAVEEL 447

AVR A L ++LLSPACAS D +++FE RG F + + ++

Sbjct: 416 AVRSAEALG--ATSLLLSPACASFDQYRDFEARGDHFQQLIHQV 457

sp Q929Y1 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 455
MURD_LISIN 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Listeria
innocua]

Score = 156 bits (395), Expect = 6e-37

Identities = 127/454 (27%), Positives = 213/454 (45%), Gaps = 34/454 (7%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTR---ENPPELATLRAQYPQVEVRCGELDAEFL 67

+V+GL +SG+S + + G V D + ENP L ++V CG E L

Sbjct: 13 LVLGLARSGVSAATIMHKLGAFTVNDQKPFSENPEAQGLLEQG--IKVICGSHPIELL 69

Query: 68 CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126

EL + +PG+ P + +A + + +++L + ++APIV ITG+N K+T TT+

Sbjct: 70 DEGFELVIKPNPGIPYNNPMIEKALKLKIPVITEVELAYQISEAPIVGITGTNGKTTTTTI 129

Query: 127 VGEMAVAADKRVAV-GGNLGTPALDLL--ADDIELYVLELSSFQLETCDRLNAEVATVLN 183

+ M A + ++ GN+G PA + A + +ELSSFQL ++ + N

Sbjct: 130 IHHMLNAHKENSSLLAGNIGFPASAVAENATSDQYISMELSSFQLMGVQTFKPHISVITN 189

Query: 184 VSEDHMDRYDGMADYHLAKHRIFRGARQ---VVVN----RADALTRPLIADTVPCWSFGL 236

+ E H+D + ++Y AK I + +V+N LT+ A +P

Sbjct: 190 IYEAHLDYHTDRSEYVQAKWHIQQNQTADDFLVINWDQEELKNLTKQTKAQVIP-----F 244

Query: 237 NKPDKAFGLIEEDGQKWLAFFQDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAM 296

+ G ++G + F + + + + G HN N +G+ + +

Sbjct: 245 STTORLEQGSYVQNGN--IMFDDEVIGSRDSILLPGEHNLENILASVAVAKTLGVTNEEI 302

Query: 297 LGALKAFSGLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDG 356

+ L+ F G+ HR Q+V E QG +Y+DSKATN+ +VLLAGG

Sbjct: 303 MYVLETFGKVEHRTQFVVEWQGRKFYNDKATNI----LATQSALKGFKNPVVLLAGGLD 358

Query: 357 KGADFHDLPREPVARFCRAVVLLGRDA---GLIAQALGNAVPLVRVATLDEAVRQAAELAR 413

+G F +L P + +++++ G A G + + G + + V ++ AV A +

Sbjct: 359 RGNSFDELL-PFFKNVKSILVFGETADKIGRVGKIAG--IEVHYVDDVEAAVPVAYRESA 415

Query: 414 EGDVLLSPACASLDMFKNFEERGRLLFAKAVEEL 447

GD +LLSPACAS D ++ FE RG + A+ EL

Sbjct: 416 PGDIILLSPACASWDQYRTFEVRGNAYMDAISEL 449

sp Q8Y5M1 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 455
MURD_LISMO 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Listeria
monocytogenes]

Score = 155 bits (393), Expect = 1e-36

Identities = 126/454 (27%), Positives = 211/454 (45%), Gaps = 34/454 (7%)

```

Query: 11  IVVGLGKSGMSLVRYLARRGLPFAVVDTR---ENPPELATLRAQYPQVEVRCGELDAEFL 67
      +V+GL +SG+S   + + G   V D +   ENP   L   ++V CG   E L
Sbjct: 13  LVLGLARSGVSAATIMHKLGAFTVNDQKPFSENPEAQGLLEQG---IKVICGSHPIELL 69

Query: 68  CSARELYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTL 126
      EL + +PG+   P + +A   + +   +++L + ++APIV ITG+N K+T TT+
Sbjct: 70  DEGFELVIKNPGIPYNNPMIEKALKLKIPVITEVELAYQISEAPIVGITGTNGKTTTTTI 129

Query: 127  VGEMA-VAADKRVAVGGNLGTPALDLL--ADDIELYVLELSSFQLETCDRLNAEVATVLN 183
      + M   +   + GN+G PA +   A   +   +ELSSFQL   +   ++ + N
Sbjct: 130  IHHMLNTHKENSLLAGNIGFPASAVAENATSDQYISMELSSFQLMGVETFKPHISVITN 189

Query: 184  VSEDHMDRYDGMADYHLAKHRIFRGARQ---VVVN----RADALTRPLIADTVPCWSFGL 236
      + E H+D +   ++Y AK I +   +V+N   LT+   A   +P
Sbjct: 190  IYEAHLDYHTDRSEYVQAKWHIQKNQIADDFLVINWDQEELKNLTKQTKAQVIP-----F 244

Query: 237  NKPDFKAFGLIEEDGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAM 296
      +   G   ++G   + F + +   + + G HN N   +G+ + +
Sbjct: 245  STTQRLGQGSYVQNGN--IMFNDEVIGERDNILLPGEHNLENVLASVAVAKTLGVTNEEI 302

Query: 297  LGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDG 356
      + L+ F G+ HR Q+V E QG +Y+DSKATN+   +VLLAGG
Sbjct: 303  MHVLETFGKVEHRTQFVVEWQGRKFYNDKATNI----LATQSALKGFKNPVLLAGGLD 358

Query: 357  KGADFHDLREPVARFCRAVLLGRDA---GLIAQALGNAVPLVRVATLDEAVRQAAELAR 413
      +G F +L P + + +++ G A G + + G + + V ++ AV A +
Sbjct: 359  RGNSFDELL-PFFKNVKT LIVFGETADKIGRVGKIAG--IEVHYVDNVEAAVPVAYRESA 415

Query: 414  EGDVALLSPACASLDMFKNFEERGR LFAKAVEEL 447
      GD +LLSPACAS D ++ FE RG + A+ EL
Sbjct: 416  PGDIILLSPACASWDQYRTFEVRGNAYMDAIGEL 449

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sp Q9ZDC2      UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC      445
MURD_RICPR 6.3.2.9)                                     AA
              (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
              (D-glutamic acid adding enzyme) [MURD] [Rickettsia
              prowazekii]

```

Score = 155 bits (392), Expect = 1e-36

Identities = 136/460 (29%), Positives = 198/460 (42%), Gaps = 61/460 (13%)

```

Query: 12  VVGLGKSGMSLVRYLARRGLPFAVVDTRENNP---ELATLRAQYPQVEVRCGELDAEFLC 68
      + GLGK+G+S+   L +   D N   EL   + R +LD
Sbjct: 11  IFGLGKTGISVYEELKNKYDLIVYDDLEANRDIFKELFGNNLITVLSDSRWQDLD----- 65

Query: 69  SARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAK-APIVAITGSNAKSTVTTLV 127
      ++ +SPG+ L   + A   + I DIDLF ++K   +AITG+N KST T L+
Sbjct: 66  ---KIVLSPGVPLTHEVRIAHHFNIPISDIDLFPEKSKNLKFIAITGTNGKSTTTALI 122

Query: 128  GEMAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSED 187
      + +   V GN+G PAL A + E YVLELSSFQL+   +VA +LN++ D
Sbjct: 123  SHILNSNGLDYPVAGNIGVPALQAKASN-EGYVLELSSFQLDLVKSFTVKVAVLLNITPD 181

```

Query: 188 HMDRYDGMADYHLAKHRIFRGARQVVVNADALTRPLI-ADTVPCWSFGLNKPDKAFGL 246
 H+DRY M DY AK +IF +R D + +I D C K F L
 Sbjct: 182 HLDRYQDMNDYIAAKAKIF-----DRMDKDSYAVINIDNDYC-----RKIFVL 224

Query: 247 IEEDGQ-KWLAFQFDKLLPVG-----ELKIRGAHNYSNXXXXXXXXXG 286
 +++D K + F K+L G ++G HN N
 Sbjct: 225 LQKDQSIKLIPFSVTKILKNGISIVDDKIHDNDLTYKLPLNKNLQGLHNCENIAASYAVA 284

Query: 287 HAVGLPFDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDG 346
 +GL +L ++ +F L HR Q++ +S+Y+DSKATN
 Sbjct: 285 KIIGLESKKILESISFQSLHHRMQYIGSINNISFYNDKATNAISALQSIKAL-----D 339

Query: 347 KLVLLAGGDGKGADFHDLEPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDE--- 403
 + LAGG K ++ P + G+ + A N + V L+
 Sbjct: 340 NIYWLAGGIPKEGGIEGIK-PYFNKIKKAYFYGQAKAMFANTAKNIIDFVICDNLEYAFN 398

Query: 404 -AVRQAAELAREGDAVLLSPACASLDMFKNFEERGRIFAK 442
 A + A E +LL+P+C+S D FKNFEERG LF K
 Sbjct: 399 IAYKDAVSDTTEVKNILLAPSCSSYDQFKNFEERGELFIK 438

trnew CAF20500 **UDP-N-ACETYLMURAMOYLALANINE D-GLUTAMATE LIGASE (EC 472**
6.3.2.9) [MURD] **AA**
[Corynebacterium glutamicum (Brevibacterium flavum)] align

Score = 153 bits (387), Expect = 5e-36
 Identities = 131/457 (28%), Positives = 199/457 (42%), Gaps = 41/457 (8%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V G G SG+S+ + L+ V D E + + E L S
 Sbjct: 16 LVAGAGVSGLSIAKMLSELHCDVVVADDNETARHMLIEVVDVADISTAQAQ---EQLDSF 72

Query: 71 RELYVSPGLSLRTPALVQAAKGVRIISGDIDLFAREAKAPI-----VAITGSNAKSTV 123
 + SPG + LV A +G+ + GD++L R +A + +A+TG+N K+T
 Sbjct: 73 SIVVTSPGWRPTSTLLVDAHRQGLEVIGDVELAWRLDQAGVFGEPTWLAVTGTNGKTTT 132

Query: 124 TTLVGEMAVAADKRVAVGGNLGTPALDLLA--DDIELYVLELSSFQLETCDRNLNAEVATV 181
 T+++ M GN+G P + L + I++ V ELSSFQL + V
 Sbjct: 133 TSMLAAMNNEGFTAKAVGNIGIPVSEALVAKNRIDVLVAELSSFQLHWSPTFTPDAGVV 192

Query: 182 LNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNADALTRPLI--ADTVPCWSFGLNKP 239
 LN++EDH+D + M DY LAK + +G + ++ D L AD F +N+P
 Sbjct: 193 LNLAEDHIDWHGSMRDYALAKMEVLKG-KVAIIGADDPYLVQLTSEADLSGLIGFTVNPE 251

Query: 240 -----DFKAFLIEED-GQKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPF 293
 KA L++ G + D + P G + A + G+
 Sbjct: 252 ATGQLGVKAGELVDNAYGNVVLASADGINPAGPAGVLDA-----LAAA AVARSQGVAP 305

Query: 294 DAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAG 353
 +A+ AL +F HR Q V E GV + D+SKATN ++ + G
 Sbjct: 306 EAIARALDSFEVAGHRGQVVAEHDGVHFIDNSKATNPHAADSALAG-----HDSVIWVVG 360

Query: 354 GDGKGADFHDLEPVARFCRAVVLLGRDAGLIAQALGNAVPLVRV-----ATLDEA 404
 G KGAD L + + +A ++LG D I AL V ++E
 Sbjct: 361 GQLKGADIAPLVKKHEQRIKAALVLGADRAEIVAALKEHASQASVFVTDKTEPFEEAMEEI 420

Query: 405 VRQAAELAREGDAVLLSPACASLDMFKNFEERGRLFA 441
V +A ++ GD VLL+PA ASLDMFK +RG LFA
Sbjct: 421 VTEAFSISEPGDTVLLAPAAASLDMFKMGQRGDLFA 457

sp Q821S1 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 419
MURD_CHLCV 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Chlamydomophila
caviae]

Score = 152 bits (385), Expect = 8e-36
Identities = 127/450 (28%), Positives = 203/450 (44%), Gaps = 55/450 (12%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
IV+G G +G S+ +L RG +D L L + C +L +
Sbjct: 7 IVLGAGVTGKSVAEFLHSRGSYVIGIDG-----SLDALNS-----CSFFHERYLDTI 53

Query: 71 RE-----LYV-SPGLSLRTPALVQAAAKGVRISGDIDLFAREA---KAPIVAITGSNAK 120
E L+V SPG+ +V+A +G+ I D+ L ++ + P + ITGS K
Sbjct: 54 EEFPEDMDLFVRSPGVKPSHSLVVEAKRRGIPIVTDVQLAFQDPEFHRYPSIGITGSAGK 113

Query: 121 STVTTLVGEMAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSFQLETCDRLNAEV-- 178
+T + + + GN+G P L + + + V+E+SSFQ L T + V
Sbjct: 114 TTTVLFLVHLLRSMGMGAFAMGNIGVPILQAMREK-GIRVVEISSFQ L-TEQEIETPVLS 171

Query: 179 -ATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLN 237
A +LN+SE+H+D + + +Y AK I + + V L
Sbjct: 172 GAAILNISENHLDYHQSLQNYSEAKRNIKCLQSVE-----SLW 210

Query: 238 KPDFKAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAML 297
++ + G D K +A DK + L + NY +P +A L
Sbjct: 211 VGEWLSPGKSYLDYTKETIASVLDKGSALKPLYLHDRSNYC--AAYALANEISNVPLEAFL 268

Query: 298 GALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGLVLLAGGDGK 357
AL+ F HR +++ E+ GVS Y +DSKAT + ++ +++ GG K
Sbjct: 269 QALQTFEKPPHRIEYLGEKDGVS YINDSKATTMSSVEKALIAVKENV---IVILGGRNK 324

Query: 358 GADFHDLREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREGDA 417
G+DF L + + + +V +G IAQAL ++PL + L EAV A +A+ GD
Sbjct: 325 GSDFTSLIPILTQTVKHIVAMGECRNEIAQALSGSLPLTQARDLQEAVSMAQSIAPGDV 384

Query: 418 VLLSPACASLDMFKNFEERGRLFAKAVEEL 447
+LLSP CAS D F++FEERG F + V ++
Sbjct: 385 ILLSPGCASFDQFRSFEERGDCFRQLVGDM 414

sp P73668 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 452
MURD_SYNY3 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Synechocystis
sp. (strain PCC 6803)]

Score = 152 bits (383), Expect = 1e-35

Identities = 129/445 (28%), Positives = 203/445 (44%), Gaps = 22/445 (4%)

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Query: 12  VVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQ--VEVRCGE-LDAEFLC 68
          V+GLG+SG++ R L R G   V D +N +L +   Q + ++ G+ LD
Sbjct: 6   VIGLGRSGIAAARVLHRDQWQVTVFDQADND-QLRHMGQPLVQEGISLKLGDRLDPVKEA 64

Query: 69  SARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKA-PIVAITGSNAKSTVTTLV 127
          + VSPG+   P LV A   KGV ++G+++L +   A P V ITG+N K+T T+LV
Sbjct: 65  WPERIVVSPGVPWDIPLLVAAREKGVEVTGELELAWQYLHAVPWVGITGTNGKTTTTSLV 124

Query: 128  GEMAVAADKRVAVGGNLGTPALDLLADD--IELYVLELSSSFQLETCDRLNAEVATVLNVS 185
          + A       GN+G A +L+ +   + V E+SS+Q+E+ L ++   +
Sbjct: 125  QAIFQKAGLNPACGNIGYAACELVLQNQNYDWIVAEISSYQIESSPTLAPQIGLWTTFT 184

Query: 186  EDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFGLNKPDKAFG 245
          DH+ R+ + +Y K + +   V+N D   + P + +   G
Sbjct: 185  PDHLNRHKTLENYFNKASLLSRSAIQVLNGDDPHLHSHGPNLYPQAHWTSTQGANHLA 244

Query: 246  LIEEDG-----QKWLAFQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGAL 300
          L +           W+   + + P+   K+ G HN N   G+ A+ L
Sbjct: 245  LCDPKQGVYLQDNWVNAFGELIAPINLFKMPGQHNQQLLMAIAAARLAGIDKKAITETL 304

Query: 301  KAFSGLAHCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGAD 360
          F+G+ HR + +   GV + +DSKATN   + G +L+AGG+ K D
Sbjct: 305  LTFTGVPHRLEPICTINGVQFINDSKATN----YDAAEVGLSSMKGPTILIAGGEAKEGD 360

Query: 361  FHDLREPVARFCRAVLLGRDAGLIAQALGNAVPLVR---VATLDEAVRQAAELAREGD- 416
          + +   AV+L+G A A L AV   V T+ AV++ ELA + +
Sbjct: 361  DQAWLAQIRQKAVAVLLIGDAAPNFATRL-KAVGYENYEIVETMANAVQRGLELASKNNA 419

Query: 417  -AVLLSPACASLDMFKNFEERGRLF 440
          AVLLSPACAS D + +FEERG F
Sbjct: 420  SAVLLSPACASFDQYNSFEERGEDF 444

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trnew CAE50125 Putative UDP-N-acetylmuramoylalanine-D-glutamate ligase 480
          [DIP1600] AA
          [Corynebacterium diphtheriae] align

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Score = 150 bits (378), Expect = 5e-35

Identities = 129/463 (27%), Positives = 208/463 (44%), Gaps = 38/463 (8%)

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Query: 11  IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
          +V G G SG+ + + L G   V D+ N +L L Q   + ++ ++
Sbjct: 25  LVAGAGVSGVGITQLLREMGCATVADS--NSAQLDKLAQQTGCQTISPADVVSDFQDY 82

Query: 71  RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPI-----VAITGSNAKSTV 123
          + SPG   +P LV A + G+ + GD++L R +A +   + +TG+N K+T
Sbjct: 83  TVVVTSPGWRPDSPLLVAQASAGLEVIGDVELVYRLDRAEVFGPKRTWMVVTGTNGKTTT 142

Query: 124  TTLVGEMAVAADKRVAVGGNLGTPALDLLADD--IELYVLELSSSFQLETCDRLNAEVATV 181
          T ++ E+ + R A GN+G D + I++ V ELSSFQL L +V +
Sbjct: 143  TAMLAIEIMQHSGARAAAVGNIGVSVADAVRTQPRIDVLVAELSSFQLHWSSTLVPDVGIL 202

Query: 182  LNVSEDHMDRYDGMADYHLAKHRIFRGARQV-----VVNRADALTRPLIADTVPCWSF 234
          LN+++DH+D + A Y K ++   + V+   + R AD P F

```

Sbjct: 203 LNLADDHIDWHGSFAQYAQDKAKVLAAPTAIAGFDNGHVMETETTRIQAEDAD--PIIGF 260

Query: 235 GLNKPDKAFGLIEEDGQKW-LAFQFDKLLPVGE-LKIRGAHNYSNXXXXXXXXGHAVGLP 292
L +P G+ DGQ AF + +L E ++ G ++ ++G+

Sbjct: 261 TLGEPAGKMGVGV--RDGQLIDCAFGDNNVLRSAEGIEPAGPAGLNDALAAAAAARSMGVS 318

Query: 293 FDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLA 352
+ AL F HR Q V + V D+SKATN +V +A

Sbjct: 319 AVCIEEALSKFEVAGHRGQCVGRHREVVAIDNSKATNPAAADSALAGFSS-----VWVVA 373

Query: 353 GGDGKGADFHDLEPVARFCRAVLLGRDAGLIAQALGNAVPLVRVAT-----LDE 403
GG KGA+ +L A +AV LLG D +I ++ +P + V + +DE

Sbjct: 374 GGQLKGAIDELIVRHAGRIKAVALLGVDREVIEDSVRTHIPGIPVLSVSETDPRRAMDE 433

Query: 404 AVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLLFAKAVEE 446
AV + A GDA++L+PA ASLDM+ +RG +FA A+ +

Sbjct: 434 AVAWSVSQAEAGDAIVLAPAAASLDMYTMGMQGRGDMFATAIAQ 476

trnew AAS08792 **UDP-N-acetylmuramoylalanine--D-glutamate ligase [LJ0971]** 460 AA
[*Lactobacillus johnsonii*]
[align](#)

Score = 149 bits (377), Expect = 7e-35
Identities = 129/457 (28%), Positives = 207/457 (45%), Gaps = 32/457 (7%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
+++GLGKSG S+ + L + G + D ++ + V V G E

Sbjct: 13 LILGLGKSGFSVAKLLLKLAKLTLNDKKDLSDNDRAAELGKLGVRVISGYHPVEIFDEE 72

Query: 71 RELYV--SPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVG 128
+ Y+ +PG+ P + +A + + + ++ ++AP V +TGSN K+T L

Sbjct: 73 KFDYLVKNPGIPYENPMVEKAEKLDIPVITEPEIALNVSEAPYVCVTGNSGKTTTVMMLTQ 132

Query: 129 E-----MAVAADKRVAVGGNLGTPALDLL--ADDIELYVLELSSFQLETCDRLNAEVATV 181
++ AVG N+G P +++ A +L V+E+SSFQL + +VA +

Sbjct: 133 RIMDHNLKNGGHAYAVG-NIGVPISEVVEKATSKDLLVEMSSSFQLLGVTDIKPKVAAI 191

Query: 182 LNVSED-HMDRYDGMADYHLAKHRIFRGARQVVNRADALTRPLIADTVPCWSFGLNKP 240
+++ + H+D + +Y AK RI + Q A+ + ++ L+K

Sbjct: 192 VDIYNNVHLDYHKTFDNYVEAKLRITQSQDQDDYFIANFDQKNILEKE-----LDKTK 244

Query: 241 FKAFLGIEED-----GQKWLAQFDK-LLPVGELKIRGAHNYSNXXXXXXXXGHAVGLP 292
K E D G ++L + D ++ + ++KI G HN N +G

Sbjct: 245 AKVQTFSETDKTADYFIGDEYLESKDDHHIMKISDIKIPGIHNQQNCLVAIAISKLMGAD 304

Query: 293 FDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLA 352
+ AL F+G HR Q+V Y+DSK+TN+ VL+A

Sbjct: 305 DSDIQYALSTFTGATHRLQYVMTYNDRIYNDKSTNIEAATVAIPSFKEPE---VLIA 360

Query: 353 GGDGKGADFHDLEPVARFCRAVLLGRDAGLIAQALGNA--VPLVRVATLDEAVRQAAE 410
GG +G F L + +++VL G L+A A A +V V TL EAV +A E

Sbjct: 361 GGLDRGFMFDSLVPFLFKKHVKSIVLYGETKYLLADAARKAGIKDIVIVNTLQEAVPAYE 420

Query: 411 LAREGDAVLLSPACASLDMFKNFEERGRLLFAKAVEEL 447
L+ GD +L SPACAS D F FEERG F K ++EL

Sbjct: 421 LSEAGDVILFSPACASWDQFNTFEERGDFFVKFIKEL 457

trnew CAE77734 **MurD protein (EC 6.3.2.9) [MURD] [Bdellovibrio** 418
bacteriovorus] AA
align

Score = 148 bits (373), Expect = 2e-34

Identities = 128/444 (28%), Positives = 197/444 (43%), Gaps = 43/444 (9%)

Query: 15 LGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSARE-- 72
 +GKSG + R L G P + T + + R D + L + +
 Sbjct: 1 MGKSGEAAKRLTLTAG-----HAPESILTFDGKLESAQFR----DPQVLMNQKPGT 47

Query: 73 LYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAP-IVAITGSNAKSTVTTTLVGEMA 131
 L VSPG+ L + + A GV+I+ ++ L + ++ +TGS KST +++G
 Sbjct: 48 LVVSPGVPLASAWIQDARKNGVQITSELSLACATLETEKMIGVTGSVGKSTTVSILGAGL 107

Query: 132 VAADKRVAVGGNLGTPALDLLADDIE-----LYVLELSSFQLETCDRLNAEVATVLNV 184
 A K VGGNLGTP D AD IE +LELSS+QLE C+ L+ + + + +
 Sbjct: 108 EAFSKTGfVGGNLGTPFADYAADVIEGKRPRADWVILELSSYQLENCEGLSLDYSAITYL 167

Query: 185 SEDHMDRYDGMADYHLAKHRIFRGARQVVNRADALTRPLIADTVPCWSFGLNKPDKAF 244
 + +H++RYD + Y+ K +I + ++ + D V + K
 Sbjct: 168 TSNHLERYDNLQHYYDTKWKILSLTKDALLNREG-----GDLVEYFHKNGQPEQVK-- 219

Query: 245 GLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFS 304
 +I + + Q +K +G+ HN N + P A+ G +K+F
 Sbjct: 220 -IISRDKMLTSLQLEKAQLIGQ-----HNQDNLALASALASAKWPASAIEG-MKSEFK 271

Query: 305 GLAHRQCQVWRERQGVSYDDSKATNVXXXXXXXXXXXXDID--GKLVLLAGGDGKGADFH 362
 GL HR + V +G+ + +DSKAT + + G+L LL GG K +
 Sbjct: 272 GLVHRLESVGTYKGIRFINDSKATAMDSVLIATAAAHDTLSKPGRLWLLLGGRDKNLPWQ 331

Query: 363 DLREPVARFCRAVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAELAREGDAVLLSP 422
 DL+ V G + IAQ + +P A L EA+ A+ GD VLLSP
 Sbjct: 332 DLKALGNLKDIEFVFFG-ECREIAQTK-STLPGRSFARLGEALCDILGSAKPGDTVLLSP 389

Query: 423 ACASLDMFKNFEERGRLLFAKAVEE 446
 SLD FK+FE+RG F K V E
 Sbjct: 390 GGTSLDEFKSFEDRGNYFKKCVSE 413

tr Q7V5V5 **UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)** 460
[MURD] AA
[Prochlorococcus marinus (strain MIT 9313)] align

Score = 147 bits (371), Expect = 3e-34

Identities = 131/467 (28%), Positives = 208/467 (44%), Gaps = 50/467 (10%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRA--QYPQVEVRCG---ELDA- 64
 +VVGLG+SG+ R L G V++ R P L +L A + + V G EL++
 Sbjct: 5 VVVGLGRSGIGAARLLQAEGHQVTVLE-RSIEPHLQSLAADLRLQGIARELKGKPLELNSF 63

Query: 65 -EFLCSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFARE-AKAPIVAITGSNAKST 122

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      L      + +SPG++  P L      +G+ I G++ +  R  +  P +AITG+N K+T
Sbjct: 64  IPLLDQLDAVVISPGIAWDHPTLTALRQRGIDIDGEMAVAWRSLSHLPWIAITGTNGKTT 123

Query: 123  VTTLVGEMAVAADKRVAVGGNLTGTPALDLL-----ADDIELYVLELSSSQLETCDRLN 175
      VT L+  +  +  R  +GGN+G  A  ++      A  +  V+ELSS+Q+E  +
Sbjct: 124  VTHLLNHVLESNGLRAPMGGNVGHAAAEVALKWRQPNAQRPDWLVMELSSYQIEAAPEIA 183

Query: 176  AEVATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRADALTRPLIADTVPCWSFG 235
      +      N++ DH++R+  +  Y  K  +  +  +  N  D  P  +      W  G
Sbjct: 184  PRMGIWTNLTPDHLERHGTLDAYRTIKRGLLERSEIRIFNGDD----PDLRSQRSSWDKG 239

Query: 236  L-----NKPDP--KAFGLIEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXX 282
      L      ++ DF  A GL+ E      L      L  +  G  HN  N
Sbjct: 240  LWVSSEPGGTANHRADFWDIAEGLVREPQ-----GALFAASALAMPGQHNLQNLILLV 291

Query: 283  XXXGHAVGLPFDAMLGALKAFSGLAHRQWVRERQGVSYDDSKATNVXXXXXXXXXXXXX 342
      GLP  A+  +L++F G+ HR  +  +  Q  +S Y+DSKATN
Sbjct: 292  TAAARQTGLPAKAIEASLRSFPGVPHRLEQLGHIQQMSVYNDSKATNYDAACVGLKA--- 348

Query: 343  DIDGKLVLLAGGDGKGADFHDLPREVARFCRAVVLLGRDAGLIAQAL---GNAVPLVRVA 399
      +      V+LAGG K  D      +  +  +  AV+L G  A  +  +  +  G  +  L  +
Sbjct: 349  -VPPPAVVLAGGQTKQGDSAGWLKQLDQACAVILFGAGASELQELIKTSGFSGELHCCS 407

Query: 400  TLDEAVRQAELA--REGDAVLLSPACASLDMFKNFEERGRLEFAKAV 444
      L+ AV  A  L  R+  +LLSPACAS D +++FE RG  F  +
Sbjct: 408  NLNAAVTLAIPLGVERQAACLLLSPPACASFDQYQDFEARGEHFRSLI 454

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sp   Q8G4Q6      UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC      481
      MURD_BIFLO 6.3.2.9)      AA
      (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)      align
      (D-glutamic acid adding enzyme) [MURD] [Bifidobacterium
      longum]

```

Score = 147 bits (370), Expect = 4e-34

Identities = 134/494 (27%), Positives = 208/494 (41%), Gaps = 79/494 (15%)

```

Query: 6  SDHFRIVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAE 65
      +D  ++ GLG SG SL  L  RG      VD R+  +L  +      +V  +D
Sbjct: 4  ADKTVVIAGLGVSGTSLAEVLRERGRTHVIGVDERKPEADLHSFD-----DVDWDHVDY- 56

Query: 66  FLCSARELYVSPGLSLRTPALVQAAAGVVRISGDIDLFAREK-----APIVAITG 116
      +  SP  + RTP +++A  +G+  +  +++ FA  +  +      AP  +  ITG
Sbjct: 57  -----VMSSPVFNPRTPFVLEAQRGIPVMSEVE-FAWQLRVNNERTGTPAPWIGITG 108

Query: 117  SNAKSTVTTLVGEMAVAADKRVAVGGNLTGTPALDLLADDI-----ELYVLELSSSQLET 170
      +N K++ T  +  EM  A      GN+  +  +  +      ++  +ELSSQFL
Sbjct: 109  TNGKTSTTEMTSEMLTACGLDAPTAGNIASGDMMSLSRCATNPQHDVLCVELSSQFLHF 168

Query: 171  CDRLNAEVATVLNVSEDHMDRYDGMADYHLAKHRIFRGA-RQVVVNRADALTRPLIADTV 229
      D L  +  A  +  N+++DH+D  +  G  +Y  K  ++F  A  R  +V  N  DA  L  A+
Sbjct: 169  TDSLALDCAAITNIADHDLDWHGGRENYAADKSKVFHNAKRAIVYNAQDAKVSELAEEAQ 228

Query: 230  PC-----WSFGLNKPDPFKAFGLIEEDGQKWLA-----FQFDKLL-P 264
      F  L  P      G+  EDG  W+      F  L  P
Sbjct: 229  TAEGCRKVGFTLEAPQAGQIGI--EDG--WIVDRSGVAGGAVGESVRLAAITDFTHLAEP 284

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Query: 265 VGELKIRGAHNYSNXXXXXXXXGHAVGLPFDAMLGALKAFSGLAHRCQWVRERQ---GVS 320
G L H ++ +G D L AL +F HR + V E V
Sbjct: 285 DGSLY---PHLVADVLTALALVLGLGADRDTALKALTSFKPGGHRIETVAEAAVEGGSVR 341

Query: 321 YYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADFDLREPVARFCRAVVLLGR 380
+ DDSKATN ++ +AGG KG+ F DL + A +A V++G+
Sbjct: 342 FVDDSKATNGHAARASLSFPAK--SVIWIAGGLAKGSRFEDLVKDQAHTIKA AVIIGK 398

Query: 381 DAGLIAQALGNAVPLVRV-----ATLDEAVRQAAELAREGDAVLLSPACASLDMFK 431
D + +A + P + V +D AV A GD VL++PACAS+D FK
Sbjct: 399 DQQPMIEAFASQAPDIPVTIIDPEDNDTVM DRAVEACGTAAAGDIVLMAPACASMDQFK 458

Query: 432 NFEERGRLFAKAVE 445
++ +RG FA A +
Sbjct: 459 SYADRGNRFAAAAK 472

sp Q9RRJ4 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 457
MURD_DEIRA 6.3.2.9) AA
(UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
(D-glutamic acid adding enzyme) [MURD] [Deinococcus
radiodurans]

Score = 145 bits (367), Expect = 1e-33

Identities = 133/453 (29%), Positives = 200/453 (43%), Gaps = 50/453 (11%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
++ GLG+SG + +L G+ D R P + A +R + G A+ +
Sbjct: 28 LIYGLGRSGRGVAHFLHGEGVSAFWHDLRPAPEDALMR-----QLGHRQADLGTTY 79

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAR-EAKAPIVAITGSNAKSTVTTLVGE 129
+ +PG+ + L A +G I G++ L AR + P+V ITG+ K + T L+ +
Sbjct: 80 DLVVAAPGPVIDHRDLRVLARGAEIIGEVALAARLRPELPMVGITGTAGKGSTTVLIAQ 139

Query: 130 MAVAADKRVAVGGNLGTPALDLLADDIELYVLELSSFQLETCDRNLNAEVATVLNVSEDHM 189
+ A R GGN+ P LD++ DD E+ V+ELSSFQLE L VA + N+ DH+
Sbjct: 140 LLRACGLRAREGGNIDPPLLDVV-DDAEVAVVELSSFQLERVPGLRLPVAVITNLGVDHL 198

Query: 190 DRYDGMADYHLAKHRIFRGAR--QVVVNRADALTRPLIADTVPCWSFGLNKPDKAFGLI 247
DR+ + YH AK I G + V+V AD L P A TV F L
Sbjct: 199 DRHGSVETYHAAKLNITAGQQSGDVLVRPAD-LPVPTRAQTV-----TFTPERLC 247

Query: 248 EEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXGHA----VGLPFD--AMLGALK 301
DGQ ++LPV +L G H +N A +G D + AL+
Sbjct: 248 LRDGQ-----EVLVPADLP-PGVHP-ANAAAALLAAEALLRHLGRAVDPAVLADALR 297

Query: 302 AFSGLAHRCQWVRERQVSYDDSKATNVXXXXXXXXXXXXDIDGKLVLLAGGDGKGADF 361
A + R + V + V + +DS AT I L GG KGA+
Sbjct: 298 AAQPVKGRFETVGQLGEVGFIEDSIATRTI AVESALRQARPPI----AWLVGGRDKGAEL 353

Query: 362 HDLREPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVATLDEAVRQAAELAREG----- 415
LR V+ G D +A+ LG +++ T DE++ +A E
Sbjct: 354 APLRAAAEGRVTRVIAFGEDGEALARDLGLPFEVIKAETGDESMDRAVRAGWEALGGAGG 413

Query: 416 -DAVLLSPACASLDMFKNFEERGRLFAKAVEEL 447

VLL+P S D F++++RG F +AV+ L
 Sbjct: 414 TGTVLLAPVGTSTFDQFRDYQQRGASFRRVQAL 446

sp Q8F7V4 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 463
 MURD_LEPIN 6.3.2.9) AA
 (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) align
 (D-glutamic acid adding enzyme) [MURD] [Leptospira
 interrogans]

Score = 143 bits (360), Expect = 6e-33
 Identities = 130/460 (28%), Positives = 204/460 (44%), Gaps = 40/460 (8%)

Query: 11 IVVGLGKSGMSLVRYLARRGLPFAVVDTRENPPELATLRAQYPQVEVRCGELDAEFLCSA 70
 +V+G G SG S + +L + D +N PE T+ +P + + L
 Sbjct: 13 LVLGGGISGNSALNFLISEKAQPILCD--QNQPE-RTVVPFFPD-----NIPPQSLPEV 63

Query: 71 RELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAKAPIVAITGSNAKSTVTTLVGEM 130
 + SPG+ P L AA K + + +IDL K I+ ITG++ KST T+L+ +
 Sbjct: 64 SLVIKSPGILPHTHPILSYAADKKIPVSEIDLGRYFFKGKIIGITGTDGKSTTTSLIAHL 123

Query: 131 AVAADKRVAVGGNLTGTPALDLLADDIELYVLELSSFQLETCDRLNAEVATVLNVSEDHMD 190
 + + GGNLG P + I L VLELSS+QLE L+ +V+ LN++ DH++
 Sbjct: 124 LKESFPDLKEGGNLGIPFTSFCKESISLAVLELSSYQLEDSSPLHLDVSVFLNLASDHLE 183

Query: 191 RYDGMADYHLAKHRI--FRGARQVVVNRA DALTRPLIADTVPC--WSFGLNKPDKAFGL 246
 R+ M +Y AK +I + ++ R L + + C SFG D AF
 Sbjct: 184 RHKTMENYFQAKLKIADLSNSNHTLIVSEKIKERILNSISYQCKLLSFG-KTSDSNAF-- 240

Query: 247 IEEDGQKWLAQFDKLLPVGELKIRGAHNYSNXXXXXXXXXGHAVGLPFDAMLGALKAFSGL 306
 ++E+ K +F + + + + G HN N +G +++ + F GL
 Sbjct: 241 LDENSLKIKTSKF--VYDISKFYLPGTHNRENLAASILAAEEIGGKPEIQTRIPLFRGL 298

Query: 307 AHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXXIDGKLVLLAGGDGKGADFDHDLRE 366
 HR Q E+ G+S+ +DSK+TN+ +ID + L+ GG K D L
 Sbjct: 299 PHRFQIAGEKLGISFINDSKSTNL-HSMLAGMATWKNID-QTCLILGGRPKQEDLKPLYN 356

Query: 367 PVARFCRAVLLGRDAGLIAQALGNV--PLVRVATLDEAVRQAAE-----L 411
 + R VVL G + N + L V L++ + +
 Sbjct: 357 FLIRGIGCVVLFGEARATWESGIKNIIGELKLYCVENLNDTFEIFKKNIFPVPGLNKDII 416

Query: 412 AREGDAV-----LLSPACASLDMFKNFEERGRLFAKAVEE 446
 R D++ + SPACAS D +KNFEERG F V +
 Sbjct: 417 IRLSDSISISSFVFPSPACASFDQYKNFEERGNHFLSLVND 456

tr Q83HK0 UDP-N-acetylmuramoylalanine--D-glutamate ligase [MURD] 480
 [Tropheryma
 whipplei (strain TW08/27) (Whipple's bacillus)] AA
 align

Score = 142 bits (359), Expect = 8e-33
 Identities = 127/467 (27%), Positives = 203/467 (43%), Gaps = 42/467 (8%)

Query: 12 VVGLGKSGMSLVRYLARRGLPFAVV----DTRENPELATLRAQYPQVEVRCGELDAEFL 67
 ++G+G SG + L G+ V TR N L + A+Y C LD

```

Sbjct: 21  ILGIGVSGFAAADSLRELGVDTVYAPEKHTRYNKL-LDAIGARYV-----CAYLDELCE 74

Query: 68  CSARELYVSPGLSLRTPALVQAAAKGVRISGDIDLFAREAK----APIVAITGSNAKSTV 123
          + VSPG+S   P + +   + + I +I+L R           P + ITG+N K+T

Sbjct: 75  VDVDIFIVVSPGISPDNPVIKRLRDRQIPILSEIELAWRVDRKVNTCPWILITGTNGKTTT 134

Query: 124  TTLVGEMAVAADKRVAVGGNLGTPALDLLADD--IELYVLELSSFQLETCDR-----LNA 176
          L G M           RVAV GN+GTP LD + +   + +V+ELSSFQL           +

Sbjct: 135  ALLTGSMIAKDGARVAVCGNIGTPVLDAVRNPKGFDYFVVELSSFQLSLLPMHGNGAVKG 194

Query: 177  EVATVLNVSEDHMDRYDGMADYHLAKHRIFRGARQVVVNRAD-----ALTRPLIADTVP 230
          + +N+ EDH++ +   Y+ AK R++ G   V   D           + + +A V

Sbjct: 195  FSSACVNLDEDHLEWHGAKELYRRAKSRVYHGTTGFCVYNLDDEETKKMVEQACVARNVR 254

Query: 231  CWSFGLNKPDKFAFGLIEE-----DGQKWLAFQFDKLLPVGELKIRGAHNYSNXXXX 282
          FGL PD   G+++           +K A +   + + + K+   H S+

Sbjct: 255  AIGFGLCVPDVGVGIVDGILCDRAFLSARKDSALEITSVEKLEKNKLSMRHIISDVLCA 314

Query: 283  XXXGHAVGLPFDAMLGALKAFSGLAHRCQWVRERQGVSYDDSKATNVXXXXXXXXXXXXX 342
          +V           ++ AL F   HR + V +   GV + +DSKATN

Sbjct: 315  VALARSVETNPLSISRALDEFCLSPHRTEVVAKEMGVMWVNDKATNPHAVIASLSNFS- 373

Query: 343  DIDGKLVLLAGGDGKGADFHDLPVARFCRAVVLLGRDAGLIAQALGNAVPLVRVAT-- 400
          +++L+ GG   KG D   + +   +AVV++G++   +   + + +

Sbjct: 374  ----RVILIFGGLMKGVDVSGIFDRFYETIKAVVIGKNQSFVGNICKKIVCIPDSNDP 429

Query: 401  LDEAVRQAAELAREGDAVLLSPACASLDMFKNFEERGRLEFAKAVEEL 447
          + EAV A LA GD VLLSP +S D F+++E RG F AV++L

Sbjct: 430  MSEAVAAADLLATPGDVTLLSPGGSSFDQFESYEHRGNCFINAVKDL 476

```

Database: EXPASY/UniProt

Posted date: Mar 28, 2004 3:51 AM

Number of letters in database: 454,374,568

Number of sequences in database: 1,423,080

Lambda	K	H
0.322	0.138	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 448

length of database: 454,374,568

effective HSP length: 127

effective length of query: 321

effective length of database: 273,643,408

effective search space: 87839533968

effective search space used: 87839533968

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.9 bits)

S2: 74 (33.1 bits)

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Proteomics tools	Swiss-Prot
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IPB004101: Mur_ligase_C

Cytoplasmic peptidoglycan synthetases, C-terminal

- o [Introduction](#)
- o [Block number IPB004101A](#)
- o [Block number IPB004101B](#)
- o InterPro entry [IPR004101](#) (source of sequences used to make blocks)
- o Block Maps.[\[Graphical Map\]](#) [\[Text Map\]](#) [\[Map Positions\]](#) [\[About Maps\]](#)
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- o [SIFT](#) to predict amino acid substitutions in blocks [\[About SIFT\]](#)
- o [Re-format](#) blocks as a multiple alignment

Blocks+ Database, Version 14.0, 1 October 2003
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 1100 Fairview AV N, Seattle, WA 98109, USA
 Please cite: S Henikoff & JG Henikoff (1991) Automated assembly of
 protein blocks for database searching, Nucleic Acids Res. 19:6565-6572.

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Block IPB004101A

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ID  Mur_ligase_C; BLOCK
AC  IPB004101A; distance from previous block=(22,577)
DE  Cytoplasmic peptidoglycan synthetases, C-terminal
BL  NDH; width=13; seqs=403; 99.5%=785; strength=1114
FOLC BACSU|Q05865 ( 164) VITSIGHDHMNIL 5
FOLC CAEEL|Q09509 ( 209) GVTTLDYDHMSIL 7
```

<u>FOLC_ECOLI</u> <u>P08192</u>	(165)	VVTSIALDHTDWL	3
<u>FOLC_HUMAN</u> <u>Q05932</u>	(220)	GVSSLGIDHTSLL	9
<u>FOLC_LACCA</u> <u>P15925</u>	(162)	VLTEVALDHQKLL	18
<u>FOLE_YEAST</u> <u>Q08645</u>	(254)	GVTLGIDHTFML	27
<u>MURC_BORBU</u> <u>O51757</u>	(187)	ILTNVDYEHVDFF	5
<u>MURC_CHLTE</u> <u>Q8KGD5</u>	(182)	VLNSLESEHMDTY	5
<u>MURC_CORGL</u> <u>P94335</u>	(191)	VVTNVEPDHLDFF	2
<u>MURC_DEIRA</u> <u>Q9RWN9</u>	(204)	VFTNAEDDHVGGE	23
<u>MURC_HELPJ</u> <u>Q9ZLL2</u>	(182)	IVPNTEPEHLEHY	17
<u>MURC_PORGI</u> <u>Q51831</u>	(180)	IITSADPDHMDIY	5
<u>MURC_STRCO</u> <u>Q9X827</u>	(182)	IVLNVELDHHANY	21
<u>MURC_TREPA</u> <u>O83361</u>	(188)	VLTSVEHDHQDYY	5
<u>MURD_BORBU</u> <u>O51532</u>	(184)	IITNVYNDHQNY	13
<u>MURD_BUCAI</u> <u>P57313</u>	(177)	VILNISEDHINRY	4
<u>MURD_MYCLE</u> <u>P57995</u>	(191)	VVLNIAEDHLDWH	2
<u>MURD_STAAM</u> <u>O33595</u>	(184)	IITNIYSAHLDYH	7
<u>MURD_SYNY3</u> <u>P73668</u>	(179)	LWTTFTPDHLSRH	16
<u>MURD_TREPA</u> <u>O83873</u>	(203)	IMTPIMADHQNWY	9
<u>MURE_BORBU</u> <u>O51219</u>	(210)	VFTNIGHEHLEFH	4
<u>MURE_DEIRA</u> <u>Q9RXL3</u>	(203)	VWTHLSSEHLDFH	16
<u>MURE_LACLA</u> <u>Q9CEN1</u>	(205)	VFLNISPDIHGPV	11
<u>MURE_TREPA</u> <u>O83903</u>	(205)	VCMNVRHEHLEFH	15
<u>MURF_BACSU</u> <u>P96613</u>	(186)	VITNIGESHMQDL	9
<u>MURF_MYCLE</u> <u>O69556</u>	(211)	VVLNVGTAHLGEF	5
<u>MURF_RICCN</u> <u>Q92H60</u>	(179)	MITNISEAHLEFF	5
<u>MURF_SYNY3</u> <u>P45450</u>	(189)	LITNVGTAHIGLL	5
<u>O68388</u>	(185)	VITNLMPTHLDYH	5
<u>CPHA_ANASP</u> <u>P58572</u>	(576)	VVLNVAADHLGIG	4
<u>CPHA_CYAA5</u> <u>Q9KGY4</u>	(578)	IVLNVAADHLGLG	5
<u>CPHA_SYNY8</u> <u>P56947</u>	(578)	VVLNVAEDHLGLG	5
<u>MPL_ECOLI</u> <u>P37773</u>	(182)	ILNNLEFDHADIF	4

MPL HAEIN	P43948	(183)	IVNNISFDHADIF	3
MUDD CHLPN	Q9Z701	(175)	VITNIDNEHLNNY	9
MURC AGRT5	Q8UDM9	(179)	VITNIDPEHLDHY	3
MURC ANASP	Q8YM75	(205)	IITNIELDHDPHY	3
MURC AQUAE	O67373	(178)	VITNVDKEHLDYF	6
MURC BRUME	Q8YI65	(179)	VVTNIDPEHLDHY	3
MURC BUCAI	P57310	(190)	IVTNIEPDHIDHY	3
MURC CAMJE	Q9PNN7	(170)	IVTNAEAEHLDHY	6
MURC CAUCR	Q9A5A6	(184)	IVTNIDAEHLDHW	19
MURC CLOAB	Q97E89	(183)	VILNIDADHLDYY	2
MURC ECOL6	Q8X9Y7	(191)	IVTNIEADHMDTY	3
MURC FUSNN	Q8RDQ2	(179)	VITNIDADHLDVH	3
MURC HAEIN	P45066	(190)	VVTNMEPDHMDTY	28
MURC MYCLE	P57994	(187)	VVTNIDSDDLDFY	2
MURC NEIMB	Q9K0Y1	(178)	VVTNIDEDHMDTY	3
MURC PASMU	P57818	(196)	VVTNIEPDHMETY	3
MURC PSEAE	Q9HW02	(187)	VVTNIDADHMATY	3
MURC RALSO	Q8XVI8	(177)	VITNIDADHMDTY	3
MURC RHIME	Q92NM0	(179)	VVTNIDPEHLDHY	3
MURC RICPR	Q9ZDS8	(185)	IITNIDPEHLDYY	2
MURC SALTI	Q8Z9G8	(191)	IVTNIEADHMDTY	3
MURC SYNY3	P74528	(229)	IVTNIELDHDPHY	3
MURC THETN	Q8R749	(181)	VILNVDSDDLDFY	3
MURC VIBCH	Q9KPG8	(194)	IVTNIEADHMDTY	3
MURC XANAC	Q8PPA7	(187)	VITNIDADHLENY	3
MURC XYLFA	Q9PF80	(187)	VVTNIDADHLENY	3
MURC YERPE	Q8ZIE8	(191)	IVTNIEADHMDTY	3
MUE1 CLOAB	Q97H84	(197)	IFTNLTQDHLDFH	2
MURE AGRT5	Q8UDM3	(197)	GFTNLGRDHMDYH	4
MURE ANASP	Q8YWF0	(203)	VFSNLTQDHLDYH	4
MURE AQUAE	O67631	(195)	LFTNLSQDHLDYH	2
MURE BACSU	Q03523	(196)	VFTNLTQDHLDYH	2
MURE BRUME	Q8YI71	(206)	AFTNLGRDHMDYH	3
MURE BUCAI	P57316	(203)	IFTNLTQDHLDYH	2
MURE CAMJE	O69290	(154)	IFTNLTQDHLDFH	2
MURE CAUCR	Q9A595	(197)	GFTNFTQDHLDYH	5
MURE CHLTE	Q8KGC9	(211)	VFTNLTPEHLDYH	3
MURE CLOPE	Q8XJ99	(197)	IFTNLTRDHLDFH	2
MURE ECO57	Q8X9Z2	(202)	VFTNLSRDHLDYH	2
MURE FUSNN	Q8R635	(193)	LFTNLTQDHLDYH	3
MURE HAEIN	P45060	(200)	IFTNLTRDHLDYH	2
MURE HELPJ	Q9ZJC6	(162)	ILTNITSDHLDFH	3
MURE LISIN	Q929X9	(195)	VFMNLSQDHLDYH	7
MURE MYCTU	O06219	(240)	AFTNLSRDHLDFH	3
MURE NEIMA	Q9JSZ0	(201)	IFTNLTRDHLDYH	2
MURE PASMU	P57815	(200)	IFTNLSRDHLDYH	2
MURE PSEAE	Q59650	(195)	VFTNLSRDHLDYH	2
MURE RALSO	Q8XVI2	(212)	LFTNLTQDHLDYH	3
MURE RHIME	Q92NL6	(199)	AFTNLGRDHMDYH	3
MURE RICPR	O05954	(189)	SFTSFSQDHLDYH	11
MURE SALTI	Q8Z9H3	(203)	VFTNLSRDHLDYH	2
MURE STAAM	Q99V74	(197)	IFSNTQDHLDFH	4
MURE STRCO	Q9S2W7	(211)	VFTNLSPEHMEFH	3
MURE SYNY3	Q55469	(213)	VFTNLTQDHLDFH	2
MURE THETN	Q8R9G2	(206)	VFTNLSQDHLDFH	2
MURE VIBCH	Q9X6N4	(206)	VFSNLSRDHLDYH	4
MURE XANAC	Q8PPB2	(198)	VFTNLTRDHLDYH	2
MURE XYLFA	Q9PF85	(198)	VFTNLTRDHLDYH	2

MURE YERPE	Q8ZIF4	(198)	VFTNLSRDHLDYH	2
MURE ZYMMO	Q9RNM2	(197)	AFTSFSRDHLDYH	5
MURC BACHD	Q9K7W1	(167)	IMTNIDFDHPDYF	5
MURC LISIN	Q92BA4	(167)	IMTNIDWDHPDYF	10
MURC STAAM	Q99TC4	(167)	IMTNIDFDHPDYF	5
MURD ECOLI	P14900	(175)	TILNVTEDHMDRY	4
MURD HAEIN	P45063	(176)	TVLNVTEDHMDRY	4
MURD RICPR	Q9ZDC2	(174)	VLLNITPDHLDYH	3
CPHA ANAVA	O86109	(576)	VVLNVAADHLGIG	4
CPHA SYNY3	P73833	(578)	VVLNVAADHLGLG	5
MUDD CHLMU	Q9PLG1	(173)	VITNIDDEHLSNF	5
MUDD CHLTR	O84767	(174)	VITNIDDEHLSNF	5
MURC BACSU	P40778	(167)	IMTNIDFDHPDYF	5
MURC BUCAP	O51926	(189)	IITNIEPDHIDNY	3
MURC ECOLI	P17952	(191)	IVTNIEADHMDTY	3
MURC HELPY	O25340	(182)	IVPNTEPEHLEHY	17
MURC LISMO	Q8Y6S8	(167)	IMTNIDWDHPDYF	10
MURC MYCTU	O06225	(187)	VITNIESDHLDFY	2
MURC RHILO	Q98KB4	(179)	VVTNIDPEHLDHY	3
MURC RICCN	Q92IT9	(185)	IITNIDPEHLDYY	2
MURC SALTY	Q8ZRU2	(191)	IVTNIEADHMDTY	3
MURC STAAU	O31211	(167)	IMTNIDFDHPDYF	5
MURC STRP3	Q8K8J5	(168)	IITNIDFDHPDYF	3
MURC STRP8	Q8P2E1	(168)	IITNIDFDHPDYF	3
MURC STRPN	Q97PS8	(169)	IITNIDFDHPDYF	3
MURC STRPY	Q9A1C7	(168)	IITNIDFDHPDYF	3
MURC THEMA	Q9WY73	(174)	IITNARGDHLENY	21
MURC XANCP	Q8PCJ9	(187)	VITNIDADHLENY	3
MURD BUCAP	Q8K9T2	(177)	VVLNITEDHLDYH	2
MURD ENTFA	O07108	(187)	VITNIFEAHLDYH	4
MURD ENTHR	O07669	(191)	VVTNIYEAHIDYH	7
MURD MYCTU	O06222	(184)	AVLNIAEDHLDWH	3
MURE BACHD	Q9K9S4	(196)	VFSNLTPDHLDYH	4
MURE BUCAP	O85298	(203)	IFTNLTQDHLDYH	2
MURE CHLMU	Q9PKC6	(199)	VLTNVSLDHLDHFH	2
MURE CHLPN	Q9Z8C5	(196)	VLTNITLDHLDHFH	2
MURE CHLTR	O84271	(196)	VLTNITSDHLDHFH	3
MURE CLOAB	Q97FC1	(201)	VFTNLSQDHLDEH	3
MURE ECOLI	P22188	(202)	VFTNLSRDHLDYH	2
MURE HELPY	O26027	(162)	ILTNITSDHLDHFH	3
MURE LISMO	Q8Y5L9	(195)	VFMNLSQDHLDYH	7
MURE MYCLE	O69557	(226)	GFTNLSRDHLDHFH	3
MURE NEIMB	Q9K0Y9	(201)	IFTNLTRDHLDYH	2
MURE RHILO	Q98KA8	(195)	GFTNLGRDHMDYH	4
MURE RICCN	Q92H59	(189)	CFTSFSQDHLDYH	8
MURE SALTY	Q8ZRU7	(203)	VFTNLSRDHLDYH	2
MURE STAAU	O86491	(196)	IFSNLQDHLDFH	4
MURE STAAW	Q8NXC2	(197)	IFSNLQDHLDFH	4
MURE STRP3	Q8K8H6	(205)	VFLNISPDIHIGPI	5
MURE STRP8	Q8P2B4	(205)	VFLNISPDIHIGPI	5
MURE STRPN	Q97PS1	(205)	VFLNISPDIHIGPI	5
MURE STRPY	Q9A196	(205)	VFLNISPDIHIGPI	5
MURE THEMA	Q9WY79	(197)	IFTNISRDHLDHFH	2
MURE XANCP	Q8PCK4	(198)	VFTNLTRDHLDYH	2
MURF ECOLI	P11880	(180)	LVNNLAAAHLEGF	4
MURF MYCTU	O06220	(209)	VVLNVGTAHLGEF	5

MURF RICPR O05953	(179)	MINNISEAHLEFF	5
MURF TREPA O83401	(194)	IITNVGCAHVGIL	14
Q9HS44	(161)	AVTSVTLEHTDVL	6
Q9HKG2	(157)	VITQVGYEHADKL	15
Q97AP2	(136)	VIAQVGYEHADKL	20
Q26630	(377)	VITNISRDHLSAG	15
Q26632	(169)	VITNLGEDHLNFH	3
Q8TXC2	(199)	VVTNVGVDHTNLV	14
Q8TXB9	(191)	CVTNITPDHLNEA	16
Q8TWI7	(190)	VLTNVSPEHLDEF	4
Q95QJ2	(220)	GVTTLDDYDHMSIL	7
Q9CAD3	(441)	VFTNLTRENTDFR	88
Q9ZHB0	(185)	VITNLMPHTIDYH	6
Q9F1N2	(180)	TCLNISEDHMDRY	5
Q54614	(161)	GITTIGLDHVALL	6
Q9EY48	(186)	IITNAGTAHVGEF	8
Q9ZHC3	(180)	IVTLVGEAHLAFF	4
Q9AKD6	(189)	SFTSFSQDHLDYH	11
Q9EY49	(195)	VFTNLSRDHLDYH	2
Q9F1M9	(204)	VVTNIEADHMDTY	3
Q9F1N5	(201)	VFTNLSRDHLDYH	2
Q9AKD7	(179)	MISNISEAHLEFF	7
Q93RQ9	(159)	VCPSIGLDHQAIL	6
Q9AKP0	(189)	CFTSFSQDHLDYH	8
Q9AKP1	(179)	MITNISEAHLEFF	5
Q8L1F3	(157)	VCPSIGLDHQAIL	6
Q9RNM3	(180)	LITAIAPAHAAFF	13
Q9F1N4	(180)	LVNNVASAHLEGF	5
Q9EY46	(180)	TVLNVSEDHMDRY	4
Q9FB03	(172)	VITNLMPHTLDYH	5
Q9KGV8	(23)	VCHNLGLDMTDVA	100
Q9RGR6	(194)	VVTNIDADHMATY	3
Q9AH11	(163)	VCPSIGLDHQAFIL	6
Q8L1G2	(163)	VCPSIGLDHQAIL	6
Q9F7N6	(180)	VINNIEFDHADIF	3
Q9AH15	(163)	VCPSIGLDHQAFIL	6
Q9X7F5	(184)	VITSISYDHETYL	23
Q9RNM7	(180)	IVTNIDPEHLDDYH	3
Q935W5	(156)	VCPSIGLDHQAIL	6
Q9L4H2	(191)	VVTNVEPDHLDFF	2
Q9FAD3	(250)	AFTNLSQDHLDFH	3
Q9AKI7	(189)	CFTSFSQDHLDYH	8
Q9AKI8	(179)	MITNISEAHLEFF	5
Q8KRM7	(170)	YITNFGKAHLEGF	29
Q8VTA5	(575)	VVLNVAADHLGIG	4
Q8L1F8	(156)	VCPSIGLDHQAIL	6
O08416	(164)	VVTPIDLDHTDRL	4
Q8GJP1	(162)	GITTIGLDHIDIL	5
Q8GE10	(228)	AFTNLTQDHLDYH	3
O83360	(205)	LLLPIEQEHTRIL	14
Q9WY13	(162)	TIVTVDRDHEKTL	35
Q9PLG7	(186)	VITHIDVQHMANF	17
Q9PLG5	(190)	MILNISDNHLDYH	10
Q9PI73	(158)	ALLPISPDHLSWH	6
Q9PGM2	(202)	ILNNLEYDHADIF	4
Q9PF84	(186)	LVNNIAPAHLERM	7
Q9PEB0	(190)	LVLNVFPEHLDWH	6
Q9KTA2	(165)	VITSLALDHTDWL	3
Q9KPG5	(206)	AFLNLSEDHMDRY	3
Q9KPG3	(180)	LVNNVAAAHALEGF	4

<u>Q9KP37</u>	(182)	VMNNLEFDHADIF	5
<u>Q9K9S8</u>	(184)	ILLNIFDAHLDYH	6
<u>Q9K9S5</u>	(185)	VVTNIGESHLEQL	8
<u>Q9K8G9</u>	(162)	IITSIGHDHMNVL	6
<u>Q9K0Y8</u>	(184)	LVNNAMRAHVGCG	15
<u>Q9K0Y4</u>	(185)	TVLNISEDHLDYH	3
<u>Q9JUE5</u>	(193)	VLNNLEFDHADIF	4
<u>Q9JSZ5</u>	(185)	TVLNISEDHLDYH	3
<u>Q9JSZ1</u>	(184)	LVNNAMRAHVGCG	15
<u>Q9JRY9</u>	(193)	VLNNLEFDHADIF	4
<u>Q9HX07</u>	(182)	ILNNLEFDHADIF	4
<u>Q9HVZ9</u>	(180)	TVLNVSEDHMDRY	4
<u>Q9HVZ7</u>	(186)	IITNAGTAHVGEF	8
<u>Q9HZA8</u>	(158)	LITSIGLDHADWL	3
<u>Q9CPB0</u>	(177)	TVLNISEDHMNRY	5
<u>Q9CMA5</u>	(185)	IINNIGFDHADIF	3
<u>Q9CIL4</u>	(179)	VITLIGEAHLEHM	8
<u>Q9CGE0</u>	(162)	GITTIGLDHIDIL	5
<u>Q9CF91</u>	(185)	LITNLFSAHLDYH	5
<u>Q9CBY8</u>	(191)	VITPVSIDHVEYL	6
<u>Q9A597</u>	(188)	VLLNISPDLDRH	2
<u>Q9A596</u>	(179)	AITTVGPVHIENF	30
<u>Q9A2L6</u>	(161)	VIAPVDLDHREFL	25
<u>Q9A0E1</u>	(163)	VCPSISFDHQERL	5
<u>Q99ZT0</u>	(163)	VCPSIGLDHQAIL	6
<u>Q99Z35</u>	(180)	VLTLVGEAHLEYF	4
<u>Q99YV3</u>	(185)	VITNLMPTHLDYH	5
<u>Q98KB1</u>	(186)	ILLNLTPDLDRH	3
<u>Q98KA9</u>	(187)	IVTMIAAAHLGFF	22
<u>Q97SW7</u>	(158)	VITSIGLDHQETL	3
<u>Q97SN7</u>	(161)	GITTIGLDHVALL	6
<u>Q97RU8</u>	(185)	VITNLMPTHIDYH	6
<u>Q97PF6</u>	(180)	IVTLVGEAHLAFF	4
<u>Q97H85</u>	(185)	LITNIGISHIENL	7
<u>Q97GG9</u>	(161)	VITSISYDHMAIL	4
<u>Q99SH5</u>	(186)	VITNIGESHMQDL	9
<u>Q92I60</u>	(174)	VLLNITPDHLDRH	3
<u>Q92DG4</u>	(185)	IITNIGEAHIEYL	3
<u>Q92BG3</u>	(165)	VITTIGMDHMEFL	5
<u>Q9JS92</u>	(173)	VFLNFSRNHLDYH	9
<u>Q8ZRU6</u>	(180)	LVNNLAAAHLEGF	4
<u>Q8ZRU4</u>	(176)	TVLNVTEHDMDRY	4
<u>Q8ZNC0</u>	(165)	VITSIALDHTDWL	3
<u>Q8ZK66</u>	(182)	ILNNLEFDHADIF	4
<u>Q8ZD24</u>	(165)	AITSIALDHTDWL	4
<u>Q8Z9H2</u>	(180)	LVNNLAAAHLEGF	4
<u>Q8Z9H0</u>	(176)	TVLNVTEHDMDRY	4
<u>Q8Z501</u>	(165)	VITSIALDHTDWL	3
<u>Q8Z145</u>	(182)	ILNNLEFDHADIF	4
<u>Q8Z0Q4</u>	(187)	VITNVGTAHIELL	5
<u>Q8YY26</u>	(155)	VITSISREHWQQL	17
<u>Q8Y8P0</u>	(185)	IITNIGEAHIEYL	3
<u>Q8Y6Y0</u>	(165)	VITTIGMDHMEFL	5
<u>Q8XJA0</u>	(188)	IITNIGISHIEIL	6
<u>Q8XJ43</u>	(161)	VLTSISLDHMNIL	4
<u>Q8XIA8</u>	(568)	VITNIREDHLGID	13
<u>Q8XHN6</u>	(246)	IITSLAEDHIGVD	10
<u>Q8XHM4</u>	(189)	IVTNITPNHLDH	12
<u>Q8XEI2</u>	(182)	ILNNLEFDHADIF	4
<u>Q8XCR3</u>	(165)	VVTSIALDHTDWL	3

<u>Q8X9Z1</u>	(180)	LVNNLAAAHLEGF	4
<u>Q8X9Y9</u>	(176)	TILNVTEDHMDRY	4
<u>Q53174</u>	(193)	VITPISIDHVDYL	6
<u>Q8UJA7</u>	(180)	IIMPISLDHEAYL	13
<u>Q8UDM4</u>	(187)	IITTIAPAHLGNF	4
<u>Q9JS38</u>	(185)	VITHINDQHMHF	25
<u>Q25439</u>	(249)	VVAEVGEQHLEYF	17
<u>Q67002</u>	(182)	LITTLGEEHLEGF	5
<u>Q67852</u>	(156)	AFISFSVDHLDWH	13
<u>Q67833</u>	(152)	GITNVERDHTRWL	12
<u>Q84761</u>	(184)	VITHIDVQHAVHF	28
<u>Q84763</u>	(173)	MILNISDNHLDYH	10
<u>P73842</u>	(156)	IITSLSREHWQVL	15
<u>Q9ZLA3</u>	(249)	VVAEVGEQHLEYF	17
<u>Q9Z707</u>	(185)	VITHINDQHMHF	25
<u>Q9WY78</u>	(162)	VLLNVGSAHLEFF	4
<u>Q9WY76</u>	(173)	LVLNISEDHLDWH	3
<u>Q9RXH3</u>	(176)	ALTNADLDHTATL	7
<u>Q9RWA1</u>	(167)	VVTTIGPAHLEQF	6
<u>Q9RRJ4</u>	(189)	VITNLGVDHLDHR	3
<u>Q9Z705</u>	(173)	VFLNFSRNHLDYH	9
<u>Q92NL7</u>	(187)	VVTSIAAAHLGNF	4
<u>Q8YI70</u>	(193)	LITLIAPAHLGHF	5
<u>Q8YI68</u>	(186)	ILLNLTPDHLDHR	3
<u>Q8XXY4</u>	(162)	VVTSVDLDHMAYL	3
<u>Q8XVP8</u>	(182)	ILNNLEFDHADIF	4
<u>Q8XVI5</u>	(246)	TILNITQDHLDDWH	3
<u>Q8XVI3</u>	(194)	LINNAQREHQEFM	19
<u>Q8RES8</u>	(161)	VITNVSLEHTEYL	3
<u>Q8RDQ1</u>	(186)	MIINIGPDHIERY	11
<u>Q8RDP8</u>	(355)	IITNIGDSHIEFL	6
<u>Q8RBN3</u>	(165)	VITSIDYDHMDKL	5
<u>Q8R9G4</u>	(181)	CIINITPDHLDHR	12
<u>Q8R6L7</u>	(568)	VITNISEDHLGID	7
<u>Q99TJ9</u>	(163)	ILTSIGLDHTDIL	3
<u>Q8PPB1</u>	(186)	LVNNIAPAHLERL	3
<u>Q8PNM5</u>	(159)	VITTVDLDDHTDWL	4
<u>Q8PII9</u>	(190)	LVLNLFPEHLDWH	6
<u>Q8PH24</u>	(183)	ILNNLEYDHADIF	4
<u>Q8PCK3</u>	(186)	LVNNIAPAHLERM	7
<u>Q8PC05</u>	(159)	VITTVDDIDHTDWL	5
<u>Q8P775</u>	(190)	LVLNLFPEHLDWH	6
<u>Q8P5P6</u>	(183)	ILNNLEYDHADIF	4
<u>Q8P1H2</u>	(163)	VCPSISFDHQERL	5
<u>Q8P154</u>	(163)	VCPSIGLDHQAIL	6
<u>Q8P0C5</u>	(180)	VLTLVGEAHLEYF	4
<u>Q8P063</u>	(185)	VITNLMPTHLDYH	5
<u>Q8NVH9</u>	(186)	VITNIGESHMQDL	9
<u>Q8NNN0</u>	(209)	AFTNLSQDHLDFH	3
<u>Q8NN38</u>	(167)	VITPVGMDHVDRL	6
<u>Q8KGD0</u>	(196)	LLTNIGHEHLEFF	5
<u>Q8KFQ9</u>	(113)	IIPSIGMDHTEWL	6
<u>Q8KCE3</u>	(187)	IINNVEFDHADIF	3
<u>Q8K7Z3</u>	(163)	VCPSISFDHQERL	5
<u>Q8K7L0</u>	(163)	VCPSIGLDHQAIL	6
<u>Q8K6X8</u>	(180)	VLTLVGEAHLEYF	4
<u>Q9S2W9</u>	(188)	AVLNLAPDHLDWH	3
<u>Q9S2W8</u>	(182)	AVLNVGSAHIGEF	5
<u>Q9L1G4</u>	(164)	VVTPIDLDHTDRL	4
<u>Q8ZIF1</u>	(176)	TILNVTEDHTDRY	4

<u>Q9F2I7</u>	(576)	VVLNVQADHLGLG	13
<u>Q8ZBA0</u>	(182)	IMNNLEFDHADIF	5
<u>Q8G4Q8</u>	(189)	IVLKVGVAHLGEF	24
<u>Q8G4Q6</u>	(178)	AITNIADDHLDWH	4
<u>Q8G4Q4</u>	(201)	IITNCEADHLDHY	28
<u>Q8G4M5</u>	(165)	IIGPVDMDHMQWL	26
<u>Q8G4M3</u>	(214)	AFLNISPDPHISPI	7
<u>Q8FZP2</u>	(186)	ILLNLTPDHLDHRH	3
<u>Q8FZP1</u>	(193)	LITLIAPAHLGHP	5
<u>Q8FZP0</u>	(195)	AFTNLGRDHMDYH	3
<u>Q8FNU1</u>	(195)	VVTNIEPDHLDFF	2
<u>Q8FNT8</u>	(196)	LVLNLAEDHIDWH	3
<u>Q8FNT6</u>	(231)	AVLVNGSAHLGEF	5
<u>Q8FNT5</u>	(223)	AFTNLSQDHLDFH	3
<u>Q8FN66</u>	(215)	VITPVGMDHTDRL	6
<u>Q8FL67</u>	(203)	VFTNLSRDHLDYH	2
<u>Q8FL66</u>	(180)	LVNNLAAAHLGEF	4
<u>Q8FL65</u>	(176)	TILNVTEDHMDRY	4
<u>Q8FFH6</u>	(165)	VVTSIALDHTDWL	3
<u>Q8FAF4</u>	(182)	ILNNLEFDHADIF	4
<u>Q8F7V4</u>	(173)	VFLNLASDHLEH	3
<u>Q8F4J4</u>	(211)	VFTNLTDHLDHFH	2
<u>Q8F4J0</u>	(182)	ILTNVDEDHLDYY	3
<u>Q8EYR2</u>	(181)	VLNALDFDHADIF	13
<u>Q8ER50</u>	(184)	VLLNLFEAHLDYH	5
<u>Q8EPN5</u>	(159)	VITTISYDHTALL	5
<u>Q8EP84</u>	(167)	IMTNIDFDHPDYF	5
<u>Q8ECR5</u>	(174)	AVTSVDLDHEAYL	8
<u>Q8EAT7</u>	(185)	VINNLEFDHADIF	3
<u>Q8E9P8</u>	(192)	VVTNIEADHMDTY	3
<u>Q8E9P6</u>	(180)	TCLNVTEDHMDRY	5
<u>Q8E9P4</u>	(180)	LVNNVNGSAHLGEF	4
<u>Q8E9P3</u>	(201)	VFTNLTRDHLDYH	2
<u>Q8E6P1</u>	(185)	VITNLMPTHLDYH	5
<u>Q8E639</u>	(180)	VVTLIGEAHLEFF	4
<u>Q8E4E0</u>	(206)	VFLNISPDPHIGPI	5
<u>Q8E3U2</u>	(169)	IITNIDFDHPDYF	3
<u>Q8E186</u>	(185)	VITNLMPTHLDYH	5
<u>Q8E0G5</u>	(180)	VVTLIGEAHLEFF	4
<u>Q8DYT2</u>	(206)	VFLNISPDPHIGPI	5
<u>Q8DY77</u>	(169)	IITNIDFDHPDYF	3
<u>Q8DVE3</u>	(185)	VITNLMPTHIDYH	6
<u>Q8DV96</u>	(181)	VVTLIGEAHLEFF	4
<u>Q8DUR4</u>	(163)	VCPSISFDHQEKL	8
<u>Q8DUG3</u>	(163)	ICTSIGLDHQAVL	6
<u>Q8DST2</u>	(207)	VFLNISPDPHIGPI	5
<u>Q8DSP4</u>	(178)	IITNIDFDHPDYF	3
<u>Q8DRE0</u>	(160)	VITSIGLDHQETL	3
<u>Q8DR92</u>	(161)	GITTIGLDHVALL	6
<u>Q8DQM2</u>	(185)	VITNLMPTHIDYH	6
<u>Q8DP40</u>	(169)	IITNIDFDHPDYF	3
<u>Q8DNV6</u>	(180)	IVTLVGEAHLAFA	4
<u>Q8DMN8</u>	(184)	LWTTLTDPHLEH	13
<u>Q8DLV5</u>	(183)	VITNIELDHPDHY	3
<u>Q8DJI4</u>	(200)	AFTNLTDHLDYH	3
<u>Q8DIM9</u>	(188)	VITNVGTAHIGRL	4
<u>Q8DEL1</u>	(194)	IVTNIEADHMDTY	3
<u>Q8DEK8</u>	(179)	AFLNLSEDHMDRY	3
<u>Q8DEK6</u>	(180)	LVNNVAAAHLGEF	4
<u>Q8DEK5</u>	(213)	VFTNLSRDHLDYH	2

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Q8DE91      ( 213) IMNNLEFDHADIF    5
Q8DB32      ( 151) VITSLALDHVDWL    4
Q8D2Z7      ( 184) VVTNIEKDHLESY   16
Q8D2Z4      ( 177) SILNVTHDHMDRY   11
Q8D2Z2      ( 182) LINNISESHLSGF    7
Q8D2Z1      ( 205) IFSNLSQDHIDYH    4
Q8D0U0      ( 191) AITSIALDHTDWL    4
Q8CZE6      ( 198) VFTNLSQDHLDYH    2
Q8CZE5      ( 187) VITNIGESHIEENL   5
Q8CZE4      ( 199) TFTNLSHEHLDYH    5
Q8CWQ5      ( 205) VFLNITPDHIGPI    5
Q8CSX6      ( 184) IITNIYSAHLDYH    7
Q8CS47      ( 167) IMTNIDFDHPDYF    5
Q8CPR2      ( 197) IFSNLTQDHLDFH    4
Q8CNZ2      ( 163) ILTSIGLDHTDIL    3
Q8CNK5      ( 186) VITNIGESHMQDL    9
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Block IPB004101B

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ID  Mur_ligase_C; BLOCK
AC  IPB004101B; distance from previous block=(0,266)
DE  Cytoplasmic peptidoglycan synthetases, C-terminal
BL  YHP; width=16; seqs=403; 99.5%=926; strength=1015
FOLC BACSU|Q05865 ( 303) LELVQEHPVYLDGAH  71

FOLC CAEEL|Q09509 ( 354) YLLDGAHTPKSMEACS  16

FOLC ECOLI|P08192 ( 299) VIFDVAHNPHAAEYLT  12

FOLC HUMAN|Q05932 ( 499) SLLLAPHPHTCSASS  73

FOLC LACCA|P15925 ( 310) IVIDGAHNPDGINGLI  14

FOLE YEAST|Q08645 ( 393) WYIDGAHTKDSMVAAS  29

MUDD CHLPN|Q9Z701 ( 318) FLEDYAHHPVEVAHTL  11

MURC DEIRA|Q9RWN9 ( 352) VVDDYAHNATKVASAV  10

MURC STRCO|Q9X827 ( 330) VVDSYAHHPTEMTADL  12

MURD BORBU|O51532 ( 198) NFDDYIIDKSKIFVNQ  66

MURD BUCAI|P57313 ( 295) VLKSFSNLPHRFQIIK  26

MURD ECOLI|P14900 ( 277) ALADAAGLPRASSLKA  15

MURD HAEIN|P45063 ( 425) RGEEFTHLAQCLTXXX  70

MURD MYCLE|P57995 ( 393) AEALSRHAPNVPVVQV  49

MURD RICPR|Q9ZDC2 ( 248) IVDDKIHNDLTYKLP  58

MURD STAAM|O33595 ( 439) IERFRAHLPSYXXXXXX  72

MURD SYNY3|P73668 ( 217) DPHLHSHGPNLYPQAH 100

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MURD TREPA	O83873	(346)	CFCASHSPAYANHAS	69
MURE BORBU	O51219	(358)	VIIDYAHTPGAFSKLF	10
MURE HELPJ	Q9ZJC6	(307)	VVVDFAHTTDGMQQVF	13
MURE LACLA	Q9CEN1	(345)	IYIDYAHNGLSLENLV	10
MURE STAAM	Q99V74	(347)	LIIDYAHTADGMNKLI	7
MURE THETN	Q8R9G2	(349)	VFIDYAHTPDGIRNIM	6
MURE TREPA	O83903	(386)	VLIDYAHTPSSFEEIL	10
MURE ZYMMO	Q9RNM2	(346)	VYVDYAHTPDGLRAAI	4
MURF MYCLE	O69556	(270)	SRGSYSHPGSPNSPDV	61
MURF SYNY3	P45450	(211)	KCELLAHQPPESTAIL	71
O68388		(199)	SFEDYVAAKWMIQAM	21
CPHA ANASP	P58572	(740)	ALVDYAHNPASYEAVG	8
CPHA CYAA5	Q9KGY4	(742)	ALVDYAHNPAGYEAVG	8
CPHA SYNY8	P56947	(742)	VLIDYAHNPAGYLAVG	8
MPL ECOLI	P37773	(326)	VYDDFAHHPTAILATL	4
MPL HAEIN	P43948	(327)	VYDDFAHHPEAILATL	4
MURC AGRT5	Q8UDM9	(333)	VFDDYGHHPVEIKAVL	4
MURC ANASP	Q8YM75	(355)	FIDDYAHHHPSEIRATL	7
MURC AQUAE	O67373	(325)	VYDDYGHHPTEIKAVI	4
MURC BACHD	Q9K7W1	(309)	LIDDYAHHHPTEISATI	4
MURC BORBU	O51757	(341)	YMDDYAHHPREIKNTL	8
MURC BRUME	Q8YI65	(332)	IFDDYGHHPVEIRAVL	5
MURC BUCAI	P57310	(347)	LIDDYGHHPTELSETI	7
MURC CAMJE	Q9PNN7	(306)	LIDDYGHHPTEIKATL	3
MURC CAUCR	Q9A5A6	(337)	VVDDYGHHPVEIAAVL	4
MURC CHLTE	Q8KGD5	(330)	VIDDYAHHHPTEVKATV	4
MURC CLOAB	Q97E89	(330)	VIDDYAHHHPTEIKATL	3
MURC CORGL	P94335	(353)	IYDDYAHHPTEVTAVL	4
MURC ECOL6	Q8X9Y7	(348)	LVDDYGHHPTEVDATI	4
MURC FUSNN	Q8RDQ2	(337)	IVDDYAHHPTEIKATL	3
MURC HAEIN	P45066	(342)	LVDDYGHHPTEVGVTI	7
MURC HELPJ	Q9ZLL2	(316)	LIDDYAHHHPTEIGATL	6
MURC LISIN	Q92BA4	(309)	LVDDYAHHPSEIRATV	5
MURC MYCLE	P57994	(349)	VFDDYAHHPTEISATL	4
MURC NEIMB	Q9K0Y1	(335)	LVDDYGHHPVEMAATL	4
MURC PASMU	P57818	(348)	LVDDYGHHPTEVGVTI	7
MURC PORGI	Q51831	(326)	LIDDYAHHHPVELDAAI	5
MURC PSEAE	Q9HW02	(339)	LVDDYGHHPREVAAVI	5
MURC RALSO	Q8XVI8	(335)	LIDDYGHHPVEMAATL	4
MURC RHIME	Q92NM0	(333)	IFDDYGHHPVEIRAVL	5
MURC RICPR	Q9ZDS8	(340)	IIDDYAHHHPPEIKATL	3
MURC SALTI	Q8Z9G8	(348)	LVDDYGHHPTEVDATI	4
MURC STAAM	Q99TC4	(309)	IVDDYAHHPREISATI	4
MURC SYNY3	P74528	(371)	FIDDYAHHHPSELLATL	7
MURC THETN	Q8R749	(329)	VVDDYAHHPAEIHATL	6
MURC TREPA	O83361	(346)	FMDDYGHHPPTAIKCTL	7
MURC VIBCH	Q9KPG8	(346)	LVDDYGHHPTEVDVTI	5

MURC	XANAC	Q8PPA7	(340)	VVDDYGHHPRELEAVF	7
MURC	XYLFA	Q9PF80	(340)	LIDDYGHHPRELEAVF	7
MURC	YERPE	Q8ZIE8	(348)	LVDDYGHHPTEVDATI	4
MUE1	CLOAB	Q97H84	(342)	VVLDYAHTPDGLEKVL	4
MURE	AGRT5	Q8UDM3	(347)	AYVDYAHKPDALENVL	5
MURE	ANASP	Q8YWF0	(353)	VIVDYAHTPDSLENLL	3
MURE	AQUAE	Q67631	(336)	VIIDYAHTPDAENVL	4
MURE	BACSU	Q03523	(348)	VIVDYAHTPDSLENVL	3
MURE	BRUME	Q8YI71	(356)	AYVDYAHKPEALENVL	6
MURE	BUCAI	P57316	(356)	FIIDYAHTPDALKKTL	6
MURE	CAMJE	Q69290	(289)	VIVDFAHTPDGIEKVL	4
MURE	CAUCR	Q9A595	(347)	AYVDYAHTPDGLQTVL	5
MURE	CHLTE	Q8KGC9	(366)	AVVDYAHTPDALQKAL	4
MURE	CLOPE	Q8XJ99	(345)	IIIDYAHTPDGLENIL	4
MURE	DEIRA	Q9RXL3	(347)	VIVDFAHTPPSLEKAL	6
MURE	ECO57	Q8X9Z2	(353)	VVVDYAHTPDALAKAL	3
MURE	FUSNN	Q8R635	(337)	VIVDYAHTPDALVNVI	5
MURE	HAEIN	P45060	(350)	VIVDYAHTPDALAKAL	3
MURE	LISIN	Q929X9	(347)	VIVDYSHTPDSLLNVL	5
MURE	MYCTU	Q06219	(389)	ALVDYAHKPEALRSVL	8
MURE	NEIMA	Q9JSZ0	(351)	VVVDYAHTPDALAKAL	3
MURE	PASMU	P57815	(350)	AIVDYAHTPDALAKAL	3
MURE	PSEAE	Q59650	(342)	VVVDYAHTPDALAKVL	3
MURE	RALSO	Q8XVI2	(367)	VVVDYAHTPDALQTL	4
MURE	RHIME	Q92NL6	(349)	AYVDYAHKPDALANVL	6
MURE	RICPR	Q05954	(334)	IFVDYSHTPDSLEKAL	5
MURE	SALTI	Q8Z9H3	(354)	VVVDYAHTPDALAKAL	3
MURE	STRCO	Q9S2W7	(359)	AVVDYAHKTDAVESVL	12
MURE	SYNY3	Q55469	(363)	VMVDYAHTPDSLENAL	4
MURE	VIBCH	Q9X6N4	(354)	MVVDYAHTPDALAKAL	7
MURE	XANAC	Q8PPB2	(348)	VVVDYAHTPDALQAL	4
MURE	XYLFA	Q9PF85	(348)	VVVDYAHTPDALQVL	7
MURE	YERPE	Q8ZIF4	(349)	VVVDYAHTPDALAKAL	3
MURF	BACSU	P96613	(328)	INDAYNASPTSMKAAI	6
MURF	RICCN	Q92H60	(329)	ICDYNASPQSMKAAL	14
CPHA	ANAVA	Q86109	(740)	ALVDYAHNPASYEAVG	8
CPHA	SYNY3	P73833	(742)	ALVDYAHNPAGYRAVG	8
MUDD	CHLMU	Q9PLG1	(314)	FLEDYAHHPSEIACITL	13
MUDD	CHLTR	Q84767	(315)	FLEDYAHHPSEISCTL	13
MURC	BACSU	P40778	(309)	LIDDYAHHPTEIKVTI	4
MURC	BUCAP	Q51926	(347)	LINDYGHHPTELSETI	28
MURC	ECOLI	P17952	(348)	LVDDYGHHPTEVDATI	4
MURC	HELPY	Q25340	(316)	LIDDYAHHPTEISATL	3
MURC	LISMO	Q8Y6S8	(309)	LVDDYAHHPSEIRATV	5
MURC	MYCTU	Q06225	(348)	VFDDYAHHPTEISATL	4
MURC	RHILO	Q98KB4	(333)	VFDDYGHHPVEISAVL	5
MURC	RICCN	Q92IT9	(340)	IIDDYAHHPPEIKATL	3
MURC	SALTY	Q8ZRU2	(348)	LVDDYGHHPTEVDATI	4
MURC	STAAU	Q31211	(309)	IVDDYAHHPREISATI	4
MURC	STRP3	Q8K8J5	(310)	IIDDFAHHPTEIVATI	5
MURC	STRP8	Q8P2E1	(310)	IIDDFAHHPTEIVATI	5
MURC	STRPN	Q97PS8	(312)	IIDDFAHHPTEIIATL	5
MURC	STRPY	Q9A1C7	(310)	IIDDFAHHPTEIVATI	5
MURC	THEMA	Q9WY73	(314)	VIDDYAHTPDEIRNLL	3
MURC	XANCP	Q8PCJ9	(340)	VVDDYGHHPRELEAVF	7
MURD	BUCAP	Q8K9T2	(295)	VLKKFLGLPHRFQTVH	63
MURD	ENTFA	Q07108	(201)	SRKEYVAAKWAIQKNM	32

MURD_ENTHR	Q07669	(296)	VAKLYGISNEAIKNAL	35
MURD_MYCTU	Q06222	(386)	AEALSRHAPDVPVQV	45
MURE_BACHD	Q9K9S4	(345)	VIVDYAHTPDSLENVL	3
MURE_BUCAP	Q85298	(356)	VIIDYAHTPDALKKAL	3
MURE_CHLMU	Q9PKC6	(345)	IYIDYAHTPDALDNVC	12
MURE_CHLPN	Q9Z8C5	(342)	VYIDYAHTPDALDNVL	4
MURE_CHLTR	Q84271	(342)	VYIDYAHTPDALDNVC	11
MURE_CLOAB	Q97FC1	(344)	IIIDYAHTPDSLEKLL	3
MURE_ECOLI	P22188	(353)	VVVDYAHTPDALKAL	3
MURE_HELPY	Q26027	(307)	VVVDFAHTIDGMQQVF	13
MURE_LISMO	Q8Y5L9	(347)	VIVDYAHTPDGLLNVL	4
MURE_MYCLE	Q69557	(375)	ALVDYAHKPGALHSVL	11
MURE_NEIMB	Q9K0Y9	(351)	VVVDYAHTPDALKAL	3
MURE_RHILO	Q98KA8	(345)	VYVDYAHKPDALNVL	5
MURE_RICCN	Q92H59	(334)	IFVDYAHTPDALKAL	3
MURE_SALTY	Q8ZRU7	(354)	VVVDYAHTPDALKAL	3
MURE_STAAU	Q86491	(346)	LIIDYAHTADGMNKLI	7
MURE_STAAB	Q8NXC2	(347)	LIIDYAHTADGMNKLI	7
MURE_STRP3	Q8K8H6	(343)	VFVDYAHNGDSLEKLL	4
MURE_STRP8	Q8P2B4	(343)	VFVDYAHNGDSLEKLL	4
MURE_STRPN	Q97PS1	(343)	VFIDYAHNGDSLKLLI	5
MURE_STRPY	Q9A196	(343)	VFVDYAHNGDSLEKLL	4
MURE_THEMA	Q9WY79	(341)	VVVDFAHSPDALEKLL	4
MURE_XANCP	Q8PCK4	(348)	VVVDYAHTPDALQAL	4
MURF_ECOLI	P11880	(357)	VVGDMAELGAESEACH	23
MURF_MYCTU	Q06220	(358)	IDDAYNANPDSMRAGL	9
MURF_RICPR	Q05953	(329)	ICDYYNASQSMKAAL	14
MURF_TREPA	Q83401	(333)	LLDCYNANPDSMAAAL	16
Q9HS44		(304)	VVLDGAHNPGACGAVA	13
Q9HKG2		(299)	IIIDAAHNPPAVNKMA	20
Q97AP2		(278)	VIIDAAHNPPAANKMV	20
Q26630		(557)	IILDYAHNPAGVRAVM	6
Q26632		(281)	VVAGKTDNPHAMRALL	64
Q8TXC2		(338)	IYDDFCHNPDGVLATV	29
Q8TXB9		(373)	VILDYGHNPAGVDATL	5
Q8TWI7		(325)	AYIDAAHNPDGLKASL	9
Q95QJ2		(365)	YLLDGAHTPKSMEACS	16
Q9CAD3		(592)	VIVDHANTPDGLSRLI	18
Q9ZHB0		(199)	LFEEYVAAKWNIQNKM	20
Q9F1N2		(379)	ALKEHSHKADSMADAV	36
Q54614		(309)	MILDGAHNPHAIKALL	8
Q9EY48		(336)	IDDSYNANPASMLAAI	6
Q9ZHC3		(321)	LSDVYNANPTAMKLIL	8
Q9AKD6		(334)	IFVDYSHTPDALKAL	4
Q9EY49		(342)	VVVDYAHTPDALKVL	3
Q9F1M9		(356)	LVDDYGHHPSEVAATI	5
Q9F1N5		(351)	IVVDYAHSPDAIEQAL	5
Q9AKD7		(328)	ICDYYNASQSMKAAL	14
Q93RQ9		(299)	LMIDGAHNNEVAALV	7
Q9AKP0		(334)	IFVDYAHTPDALKAL	3
Q9AKP1		(329)	ICDYYNASQSMKAAL	14
Q8L1F3		(297)	LMIDGAHNNEVAALV	7
Q9RNM3		(334)	IDESYNANPASMAATI	6
Q9F1N4		(328)	IDDSYNANPASVTAIV	6
Q9EY46		(299)	ALKAFSGLAHRQCQWR	30
Q9FB03		(186)	SFEDYVAAKWKMIQAM	21
Q9KGV8		(58)	IIDDFAHHPTEIEATL	3
Q9RGR6		(346)	LVDDYGHHPREVAAVI	5
Q9AHI1		(303)	LMIDGAHNNEIAVLT	10
Q8L1G2		(303)	LMIDGAHNNEVAALV	7

<u>Q9F7N6</u>	(320)	IYDDFAHHPTAIEFSS	18
<u>Q9AH15</u>	(303)	LMIDGAHNNESIAVL	10
<u>Q9X7F5</u>	(332)	VVVDGGHNPAGAAVIA	8
<u>Q9RNM7</u>	(337)	VIDDYGHHPVEIKAVL	4
<u>Q935W5</u>	(296)	LMIDGAHNNESVAALV	7
<u>Q9L4H2</u>	(353)	IYDDYAHHPTEVTAVL	4
<u>Q9FAD3</u>	(398)	AVVDYAHKPAAVAVAL	6
<u>Q9AKI7</u>	(334)	IFVDYAHTPDALKAL	3
<u>Q9AKI8</u>	(329)	ICDYNASPQSMKAAL	14
<u>Q8KRM7</u>	(311)	ILDAYNANPSSMAVAI	7
<u>Q8VTA5</u>	(739)	ALVDYAHNPMSYEALG	7
<u>Q8L1F8</u>	(296)	LMIDGAHNNESVAALV	7
<u>O08416</u>	(315)	VVLDAAHNPAGARVTA	7
<u>Q8GJP1</u>	(306)	ILLDGAHNVHAMNRL	10
<u>Q8GE10</u>	(381)	VIVDYAHTPDGLVNL	5
<u>O83360</u>	(357)	IVIDGAHTTQSIRAC	23
<u>Q9WY13</u>	(306)	YILDGAHNPHGAESLV	10
<u>Q9PLG7</u>	(329)	INDAYNASPDAMLAAL	6
<u>Q9PLG5</u>	(309)	INDSKATTVRATEKAL	19
<u>Q9PI73</u>	(195)	LPKIYANTPTKAHKIS	38
<u>Q9PGM2</u>	(348)	VYDDFAHHPTAIATTL	4
<u>Q9PF84</u>	(336)	IDDSYNANPGSLDVAI	8
<u>Q9PEB0</u>	(326)	VNDSISTTPHATLAAL	23
<u>Q9KTA2</u>	(300)	IVLDVAHNPMSAHYLV	10
<u>Q9KPG5</u>	(323)	ALKSYTGLTHRCQVVA	26
<u>Q9KPG3</u>	(330)	IDDSYNASVPAMKAAV	10
<u>Q9KP37</u>	(326)	VYDDFAHHPTAIELTL	4
<u>Q9K9S8</u>	(373)	AVVLFGETKHKLAQAA	16
<u>Q9K9S5</u>	(325)	LNDAYNASPTSMKAAI	6
<u>Q9K8G9</u>	(310)	TFVDGAHNEEGMKALA	40
<u>Q9K0Y8</u>	(332)	IDDTYNANPDSMKAAI	6
<u>Q9K0Y4</u>	(199)	DLLDYAHTKAKIFRGD	35
<u>Q9JUE5</u>	(336)	VYDDFAHHPTAIETTI	4
<u>Q9JSZ5</u>	(199)	DLLDYAHTKAKIFRGD	35
<u>Q9JSZ1</u>	(332)	IDDTYNANPDSMKAAV	7
<u>Q9JRY9</u>	(336)	VYDDFAHHPTAIETTI	4
<u>Q9HX07</u>	(326)	LYDDFAHHPTAIATTL	5
<u>Q9HVZ9</u>	(299)	ALKAFSGLAHCQWVR	30
<u>Q9HVZ7</u>	(336)	IDDSYNANPASMLAAI	6
<u>Q9HZA8</u>	(302)	LLLDVGHNPQAAQYLA	9
<u>Q9CPB0</u>	(191)	DLEDYRQAKLKIYHHA	83
<u>Q9CMA5</u>	(329)	VYDDFAHHPTAILATL	4
<u>Q9CIL4</u>	(319)	LSDVYNANPTAMRLIL	8
<u>Q9CGE0</u>	(306)	ILLDGAHNVHAMNRL	10
<u>Q9CF91</u>	(303)	VLTSFAGVKHRLQYLG	44
<u>Q9CBY8</u>	(346)	VFIDAAHNPAGANALA	8
<u>Q9A597</u>	(419)	AYADAAASGEEAIVLL	11
<u>Q9A596</u>	(333)	VDESYNANPVSMQAAL	6
<u>Q9A2L6</u>	(311)	LWLDGGHNPAGLAVS	30
<u>Q9A0E1</u>	(303)	LLLDGAHNPDSIAKLK	7
<u>Q99ZT0</u>	(303)	LMIDGAHNNESVAALV	7
<u>Q99Z35</u>	(321)	LSDVYNANPTAMRLIL	8
<u>Q99YV3</u>	(199)	SFEDYVAAKWMIAQM	21
<u>Q98KB1</u>	(333)	VNSKATNADAAAAPAL	17
<u>Q98KA9</u>	(341)	IDESYNANPASMAAAM	7
<u>Q97SW7</u>	(295)	IYLDGAHNPALTRLA	18
<u>Q97SN7</u>	(309)	MILDGAHNPAAIKALL	8
<u>Q97RU8</u>	(199)	SFSEYVAAKWNIQNKM	31
<u>Q97PF6</u>	(321)	LSDVYNANPTAMKLIL	8
<u>Q97H85</u>	(326)	VDDSYNANPDSMIAAI	7

<u>Q97GG9</u>	(310)	VVVDGAHNSDGILKLK	20
<u>Q99SH5</u>	(331)	INDAYNASPTSMRAAI	6
<u>Q92I60</u>	(447)	AYKDAVGDAEIKNIL	18
<u>Q92DG4</u>	(330)	LNDAYNSSPTALKTVL	15
<u>Q92BG3</u>	(309)	IMLDGAHNPEGVTTF	19
<u>Q9JS92</u>	(292)	INDSKATTVTAVEKAL	12
<u>Q8ZRU6</u>	(357)	VVGDMAELGAESEACH	23
<u>Q8ZRU4</u>	(278)	ALADAVGLPRASSLKA	17
<u>Q8ZNC0</u>	(299)	VIFDVAHNPHAAEYLT	12
<u>Q8ZK66</u>	(326)	VYDDFAHHPTAILATL	4
<u>Q8ZD24</u>	(311)	LILDVAHNPHAAARYLV	7
<u>Q8Z9H2</u>	(357)	VVGDMAELGAESEACH	23
<u>Q8Z9H0</u>	(278)	ALADAVGLPRASSLKA	17
<u>Q8Z501</u>	(299)	VIFDVAHNPHAAEYLT	12
<u>Q8Z145</u>	(326)	VYDDFAHHPTAILATL	4
<u>Q8Z0Q4</u>	(325)	LDETYNAAPEAMLAL	9
<u>Q8YY26</u>	(297)	LLIDGAHNPAAAHVLR	12
<u>Q8Y8P0</u>	(330)	LNDAYNSSPTALKTVL	15
<u>Q8Y6Y0</u>	(309)	IMLDGAHNPEGIKTFA	18
<u>Q8XJA0</u>	(333)	LNDAYNSSPVAVKSAI	28
<u>Q8XJ43</u>	(308)	VVIDGAHNIDGIRNLR	13
<u>Q8XIA8</u>	(732)	VILDYAHNIDGYKVVI	12
<u>Q8XHN6</u>	(407)	IILDYGHNPEAFEELF	11
<u>Q8XHM4</u>	(378)	ATVLFVGTKEKIKAAF	39
<u>Q8XEI2</u>	(326)	VYDDFAHHPTAILATL	4
<u>Q8XCR3</u>	(299)	VIFDVAHNPHAAEYLT	12
<u>Q8X9Z1</u>	(357)	VVGDMAELGAESEACH	23
<u>Q8X9Y9</u>	(278)	ALADAAAGLPRASSLKA	15
<u>O53174</u>	(348)	VFIDAAHNPAGASALA	7
<u>Q8UJA7</u>	(329)	IWIDGGHNPAGEVIA	31
<u>Q8UDM4</u>	(341)	IDESYNANPASMRAAI	6
<u>Q9JS38</u>	(327)	INDAYNACPEAMIAAL	18
<u>Q25439</u>	(436)	VFDVAIITGELNSKTI	30
<u>Q67002</u>	(318)	IDDTYNANPVSLRNAI	8
<u>Q67852</u>	(289)	YNDSKSTTPHALMHAL	26
<u>Q67833</u>	(292)	LMVDASHNPYSVVKV	27
<u>O84761</u>	(327)	INDAYNASPDAMLAL	6
<u>O84763</u>	(269)	AVATFNKPPHRMEYLG	43
<u>P73842</u>	(296)	IILDGAHNPAAAKALA	5
<u>Q9ZLA3</u>	(436)	VFDVAIITGELNSKTI	30
<u>Q9Z707</u>	(327)	INDAYNACPEAMIAAL	18
<u>Q9WY78</u>	(305)	VDDTYNASPEAFQTSI	15
<u>Q9WY76</u>	(283)	LLRDFKPLPHRMEYLG	66
<u>Q9RXH3</u>	(297)	VLVDGAHNPHAAARALA	5
<u>Q9RWA1</u>	(301)	IDDAYNASPVAVRAAL	7
<u>Q9RRJ4</u>	(276)	AEALLRHLGRAVDPAV	37
<u>Q9Z705</u>	(292)	INDSKATTVTAVEKAL	12
<u>Q92NL7</u>	(341)	IDESYNANPASMRAAI	6
<u>Q8YI70</u>	(347)	IDESYNANPTSMRAAL	5
<u>Q8YI68</u>	(200)	SMENYAAIKERLVAAS	29
<u>Q8XXY4</u>	(302)	VILDVAHNPHAAAAALG	7
<u>Q8XVP8</u>	(327)	VYDDFAHHPTAIRTTI	5
<u>Q8XVI5</u>	(393)	GLRDYAGEPHRVELIA	59
<u>Q8XVI3</u>	(344)	IDDTYNANPDSVRAAI	7
<u>Q8RES8</u>	(296)	VIFDGAHNLAGVEELI	18
<u>Q8RDQ1</u>	(200)	SFDEYYNTKFNITKNQ	78
<u>Q8RDP8</u>	(490)	INDAYNASPMSMKAAI	25
<u>Q8RBN3</u>	(308)	VVIDGAHNPPQGMTVLK	11
<u>Q8R9G4</u>	(323)	YNDSKGTNPASIKAI	16
<u>Q8R6L7</u>	(731)	VLVDYGHNVEGIKKVI	7

<u>Q99TJ9</u>	(306)	I ILDGAHNSESIDALI	17
<u>Q8PPB1</u>	(339)	IDDSYNANPGSLDAAI	7
<u>Q8PNM5</u>	(308)	VLLDVGHNPQAARALA	8
<u>Q8PII9</u>	(326)	VNDSISTTPHASLAAL	19
<u>Q8PH24</u>	(329)	VYDDFAHHPTAIATTL	4
<u>Q8PCK3</u>	(339)	IDDSYNANPGSLDAAI	7
<u>Q8PC05</u>	(298)	LMLDVGHNPQAARALA	9
<u>Q8P775</u>	(326)	VNDSISTTPHASLAAL	19
<u>Q8P5P6</u>	(329)	VYDDFAHHPTAIATTL	4
<u>Q8P1H2</u>	(303)	LLLDGAHNPDIAKLK	7
<u>Q8P154</u>	(303)	LMIDGAHNNEVAALV	7
<u>Q8P0C5</u>	(321)	LSDVYNANPTAMRLIL	8
<u>Q8P063</u>	(199)	SFEDYVAAKWWIQAQM	21
<u>Q8NVH9</u>	(331)	INDAYNASPTSMRAAI	6
<u>Q8NNN0</u>	(358)	AVVDYAHKPAAVA AVL	6
<u>Q8NN38</u>	(327)	VFIDAAHNPHGAAALG	7
<u>Q8KGD0</u>	(348)	LNDTYNANPDSVRLAL	7
<u>Q8KFQ9</u>	(259)	VMLDVSHNPEGMQKTA	8
<u>Q8KCE3</u>	(335)	LIEDFAHHPTAIRLTL	5
<u>Q8K7Z3</u>	(303)	LLLDGAHNPDIAKLK	7
<u>Q8K7L0</u>	(303)	LMIDGAHNNEVAALV	7
<u>Q8K6X8</u>	(321)	LSDVYNANPTAMRLIL	8
<u>Q9S2W9</u>	(400)	REALARHAPEVPVVDL	48
<u>Q9S2W8</u>	(334)	VNDAYNANPESTKAAL	11
<u>Q9L1G4</u>	(315)	VVLDAAHNPAGARVTA	7
<u>Q8ZIF1</u>	(293)	ALTTFSGLPHRFQLVL	25
<u>Q9F2I7</u>	(740)	VLVDYAHNPAGYEAI G	8
<u>Q8ZBA0</u>	(326)	VYDDFAHHPTAILATL	4
<u>Q8G4Q8</u>	(344)	IDDSFNANPDSMKAGL	9
<u>Q8G4Q6</u>	(382)	LVKDQAHTIKA AVIIG	34
<u>Q8G4Q4</u>	(367)	VVDDYAHHPTEIAALL	3
<u>Q8G4M5</u>	(314)	I ILDGGHNVNAAEALR	15
<u>Q8G4M3</u>	(369)	AIVDYAHNYASVTALL	29
<u>Q8FZP2</u>	(200)	SMENYAAIKERLVAAS	29
<u>Q8FZP1</u>	(347)	IDESYNANPTSMRAAL	5
<u>Q8FZP0</u>	(345)	AYVDYAHKPEALENVL	6
<u>Q8FNU1</u>	(357)	VYDDYAHHPTEVEAVL	3
<u>Q8FNT8</u>	(373)	ISELVATHAHRKAAL	14
<u>Q8FNT6</u>	(387)	INDSYNANPDSMRAGV	9
<u>Q8FNT5</u>	(372)	AVVDYAHKPAAVA AVL	6
<u>Q8FN66</u>	(375)	VFIDAAHNPHGAAALG	7
<u>Q8FL67</u>	(354)	VVVDYAHTPDAL EKAL	3
<u>Q8FL66</u>	(357)	VVGDMAELGAESEACH	23
<u>Q8FL65</u>	(278)	ALADAAGLPRASSLKA	15
<u>Q8FFH6</u>	(299)	VIFDVAHNPHAAEYLT	12
<u>Q8FAF4</u>	(326)	VYDDFAHHPTAILATL	4
<u>Q8F7V4</u>	(291)	RIPLFRGLPHRFQIAG	49
<u>Q8F4J4</u>	(365)	AVVDYAHTPDAL ENII	4
<u>Q8F4J0</u>	(363)	VYDDYGHHPTEIKAVI	4
<u>Q8EYR2</u>	(324)	VMEDFAHHPVAVHETI	11
<u>Q8ER50</u>	(217)	DYLIYNADDDNVSAAI	53
<u>Q8EPN5</u>	(300)	I IVDGAHNMEGIHSLI	21
<u>Q8EP84</u>	(308)	VIDYAHHPKEISVTI	9
<u>Q8ECR5</u>	(306)	ILLDVAHNPHAAARFLV	14
<u>Q8EAT7</u>	(332)	VYDDFAHHPTAIATTI	5
<u>Q8E9P8</u>	(344)	LVDDYGHHPSEVAATI	5
<u>Q8E9P6</u>	(264)	LIGSHNHANLLAAMAL	41
<u>Q8E9P4</u>	(333)	IDDSYNANPVSVGA AI	9
<u>Q8E9P3</u>	(351)	LVVDYAHTPDAL IEQAL	4
<u>Q8E6P1</u>	(199)	SFEDYVAAKWNIQNQM	18

<u>Q8E639</u>	(321)	LSDVYNANPTAMRLIL	8
<u>Q8E4E0</u>	(344)	IFVDYAHNGDSLKKLL	5
<u>Q8E3U2</u>	(311)	IIDDFAHHPTEIIATL	5
<u>Q8E186</u>	(199)	SFEDYVAAKWNIQNQM	18
<u>Q8E0G5</u>	(321)	LSDVYNANPTAMRLIL	8
<u>Q8DYT2</u>	(344)	IFVDYAHNGDSLKKLL	5
<u>Q8DY77</u>	(311)	IIDDFAHHPTEIIATL	5
<u>Q8DVE3</u>	(199)	SFENYIEAKWNIOKNM	32
<u>Q8DV96</u>	(322)	LSDVYNANPTAMKLIL	8
<u>Q8DUR4</u>	(303)	LLLDGAHNIDAITKLI	10
<u>Q8DUG3</u>	(303)	LMIDGAHNNEVAAALV	7
<u>Q8DST2</u>	(345)	VFVDYAHNGDSLEKLL	4
<u>Q8DSP4</u>	(320)	IIDDFAHHPTEIIATL	5
<u>Q8DRE0</u>	(297)	IYLDGAHNLPALTRLV	18
<u>Q8DR92</u>	(309)	MILDGAHNPHAIKALL	8
<u>Q8DQM2</u>	(199)	SFSEYVAAKWNIOKNM	31
<u>Q8DP40</u>	(312)	IIDDFAHHPTEIIATL	5
<u>Q8DNV6</u>	(321)	LSDVYNANPTAMKLIL	8
<u>Q8DMN8</u>	(202)	YVATKAHLMNGAKHVI	34
<u>Q8DLV5</u>	(327)	FIDDYAHHHPSEIMATL	16
<u>Q8DJI4</u>	(349)	VVVDYAHTPDLENLL	3
<u>Q8DIM9</u>	(273)	VPLAGAHHALNFLAAL	23
<u>Q8DEL1</u>	(346)	LVDDYGHHPTEVDVTI	5
<u>Q8DEK8</u>	(298)	ALKSYTGLTHRCQVVA	26
<u>Q8DEK6</u>	(330)	IDDSYNASVPAMKAAV	10
<u>Q8DEK5</u>	(361)	VVVDYAHTPDLEKAL	3
<u>Q8DE91</u>	(357)	VYDDFAHHPTAIELTL	4
<u>Q8DB32</u>	(285)	ILLDVAHNPHSAEYLV	7
<u>Q8D2Z7</u>	(342)	IVDDYGHHPTELKLT	4
<u>Q8D2Z4</u>	(294)	TLKNFSGLPFRFQIIH	36
<u>Q8D2Z2</u>	(334)	IDDSYNANVGSMISAI	12
<u>Q8D2Z1</u>	(356)	VIVDYAHTPDLEKVL	3
<u>Q8D0U0</u>	(337)	LILDVAHNPHAARYLV	7
<u>Q8CZE6</u>	(350)	VIVDFAHTPDLENVL	4
<u>Q8CZE5</u>	(331)	INDAYNASATSMKASI	12
<u>Q8CZE4</u>	(350)	IYIDYAHTPDALTKAI	5
<u>Q8CWQ5</u>	(343)	VFIDYAHNGDSLKKLI	5
<u>Q8CSX6</u>	(284)	AVLASIAGVPVKAIV	39
<u>Q8CS47</u>	(309)	IVDDYAHHPREISATI	4
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<u>Q8CNZ2</u>	(306)	MVIDGAHNNESEDALV	11
<u>Q8CNK5</u>	(331)	INDAYNASPTSMKAAI	6

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[\[Return to top\]](#)**COBBLER sequence (region containing Blocks only)**

To do a BLAST search, copy the cobbler sequence below then click on a BLAST link

[\[Blast Search\]](#) [\[Gap-Blast Search\]](#) [\[PSI-Blast Search\]](#)

COBBLER sequence:

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>IPB004101 MURC_CLOAB|Q97E89 from 173 to 355 with embedded consensus blocks
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isfnesgfssfdvykssellfnienvpqkhnlnalsaiasaltlkishksiidglksfkgthrrfeikgvkngitVID
DYAHNPFAIQAAALdaaknyphnk

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WEST Search History

DATE: Monday, March 29, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=USPT; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L1	mur.d.clm.	6
<input type="checkbox"/>	L2	mur-d.clm.	0
<input type="checkbox"/>	L3	mur near2 d.clm.	0
<input type="checkbox"/>	L4	(mur near2 d).clm.	0
<input type="checkbox"/>	L5	11 and pseudomon\$	3
<input type="checkbox"/>	L6	UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase	2
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L7	UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase	4

END OF SEARCH HISTORY

WEST Search History

DATE: Monday, March 29, 2004

Hide? Set Name Query

Hit Count

DB=USPT; PLUR=YES; OP=AND

<input type="checkbox"/>	L1	murd.clm.	6
<input type="checkbox"/>	L2	mur-d.clm.	0
<input type="checkbox"/>	L3	mur near2 d.clm.	0
<input type="checkbox"/>	L4	(mur near2 d).clm.	0
<input type="checkbox"/>	L5	11 and pseudomon\$	3
<input type="checkbox"/>	L6	UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase	2

END OF SEARCH HISTORY

[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 4 of 4 returned.**

-
- ☐ 1. [20030088061](#). 12 Oct 01. 08 May 03. Materials and methods to modulate ligand binding/enzymatic activity of alpha/beta proteins containing an allosteric regulatory site. Staunton, Donald E.. 530/350; A61K031/165 C07K014/435.
-
- ☐ 2. [20030077803](#). 09 Apr 01. 24 Apr 03. Crystals of the escherichia coli membrane-associated glycosyltransferase (MurG) protein, atomic coordinates and three dimensional structures thereof, atomic coordinates and three dimensional structures of binding domains thereof, images thereof, and methods of crystallizing MurG proteins models of UDP glycosyltransferases, MurG proteins and binding sites methods of making models, methods of using models of MurG, compounds that bind, inhibit or stimulate MurG proteins, and therapeutic compositions thereof. Walker, Suzanne, et al. 435/199; 702/19 C12N009/22 G06F019/00 G01N033/48 G01N033/50.
-
- ☐ 3. [6211161](#). 19 Mar 99; 03 Apr 01. [UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase \(MURD\)](#) (MURD) of staphylococcus aureus. Beattie; David T, et al. 514/44; 435/252.3 435/254.11 435/320.1 435/325 435/455 435/471 435/69.1 536/23.1 536/23.2 536/23.4 536/23.7. A61K048/00 C07H021/00 C12N015/31 C12N015/52 C12N015/63.
-
- ☐ 4. [6030996](#). 11 Mar 98; 29 Feb 00. Mur D inhibiting compounds, compositions containing such compounds and methods of use. Gegnas; Laura D.. 514/459; 514/460 549/216 549/217 549/218 549/219 549/417 549/418 549/419 549/420. H01N043/16 C07F009/28 C07D315/06.
-

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Terms	Documents
UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase	4

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[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 2 of 2 returned.**

☐ 1. [6211161](#). 19 Mar 99; 03 Apr 01. UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase (MURD) of staphylococcus aureus. Beattie; David T, et al. 514/44; 435/252.3 435/254.11 435/320.1 435/325 435/455 435/471 435/69.1 536/23.1 536/23.2 536/23.4 536/23.7. A61K048/00 C07H021/00 C12N015/31 C12N015/52 C12N015/63.

☐ 2. [6030996](#). 11 Mar 98; 29 Feb 00. Mur D inhibiting compounds, compositions containing such compounds and methods of use. Gegnas; Laura D.. 514/459; 514/460 549/216 549/217 549/218 549/219 549/417 549/418 549/419 549/420. H01N043/16 C07F009/28 C07D315/06.

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Terms	Documents
UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase	2

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L1: Entry 5 of 6

File: USPT

Apr 6, 1999

DOCUMENT-IDENTIFIER: US 5891621 A

TITLE: Metabolic pathway assay

CLAIMS:

10. The kit according to claim 9 wherein the first enzyme is the gene product of murC, the second enzyme is the gene product of murD, the third enzyme is the gene product of murE, and the fourth enzyme is the gene product of murF.

15. The kit according to claim 14 wherein the first enzyme is the gene product of murA, the second enzyme is the gene product of murB, the third enzyme is the gene product of murC, the fourth enzyme is the gene product of murD, the fifth enzyme is the gene product of MurE, and the sixth enzyme is the product of MurF.

29. The method according to claim 28 wherein the first enzyme is the gene product of murC, the second enzyme is the gene product of murD, the third enzyme is the gene product of murE, and the fourth enzyme is the gene product of murF.

35. The method according to claim 34 wherein the first enzyme is the gene product of murA, the second enzyme is the gene product of murB, the third enzyme is the gene product of murC, the fourth enzyme is the gene product of murD, the fifth enzyme is the gene product of murE, and the sixth enzyme is the product of murF.

37. A high-throughput in vitro screening method for detecting a biologically active compound which is comprised of:

(a) combining an enzyme cascade comprising a first enzyme, a second enzyme, a third enzyme, a fourth enzyme, a fifth enzyme and a sixth enzyme, and a labeled substrate for the first enzyme with a compound suspected of having biological activity; wherein:

the first enzyme is the gene product of murA, the second enzyme is the gene product of murB, the third enzyme is the gene product of murC, the fourth enzyme is the gene product of murD, the fifth enzyme is the gene product of murE, and the sixth enzyme is the product of murF; and

(b) measuring the concentrations of the products of the enzymes and comparing to a standard, by absorbing the product of the sixth enzyme onto resin and detecting the amount of label and comparing the amount of label to control.

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Search Results - Record(s) 1 through 6 of 6 returned.

☐ 1. Document ID: US 6534284 B1

L1: Entry 1 of 6

File: USPT

Mar 18, 2003

DOCUMENT-IDENTIFIER: US 6534284 B1

TITLE: MurD protein and gene of Staphylococcus aureus

CLAIMS:

7. A process for expressing a MurD protein of Staphylococcus aureus in a recombinant recombinant host cell, comprising: (a) transfecting a suitable host cell with an expression vector of claim 5; and, (b) culturing the host cell of step (a) in conditions under which allow expression of said the MurD protein from said expression vector.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 2. Document ID: US 6534278 B1

L1: Entry 2 of 6

File: USPT

Mar 18, 2003

DOCUMENT-IDENTIFIER: US 6534278 B1

**** See image for Certificate of Correction ****

TITLE: Screening for antibiotics

CLAIMS:

12. A method of claim 2, wherein the step of cell wall biosynthesis is the addition of D-glutamic acid to uridine diphosphate-N-acetylmuramic acid-L-alanine catalyzed by MurD.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 3. Document ID: US 6211161 B1

L1: Entry 3 of 6

File: USPT

Apr 3, 2001

DOCUMENT-IDENTIFIER: US 6211161 B1

TITLE: UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase (MURD) of staphylococcus aureus

CLAIMS:

6. An isolated polynucleotide comprising a first polynucleotide or the full complement of the entire length of the first polynucleotide, wherein the first polynucleotide encodes the same mature polypeptide, expressed by the MurD gene contained in Staphylococcus aureus WCUH 29 contained in NCIMB Deposit No. 40771.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequence	Attachment	Claims	KMC	Draw. De
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☐ 4. Document ID: US 5929045 A

L1: Entry 4 of 6

File: USPT

Jul 27, 1999

DOCUMENT-IDENTIFIER: US 5929045 A

TITLE: Recombinant expression of polynucleotides encoding the UDP-N-acetylmuramoylalanine:D-glutamate ligase (MurD) of Streptococcus pneumoniae

CLAIMS:

1. An isolated polynucleotide comprising: a first polynucleotide sequence, or the full complement of the entire length of such first polynucleotide sequence, wherein the first polynucleotide sequence (a) is a reference sequence that encodes the amino acid sequence set forth in SEQ ID NO:2, or (b) has at least 99% identity relative to a reference polynucleotide encoding the MurD polypeptide of Streptococcus pneumoniae, said reference polynucleotide consisting of nucleotides 482 to 1820 of the nucleotide sequence of SEQ ID NO:1, wherein % identity is calculated as $\frac{\text{times} \cdot 100}{N \cdot \text{sub} \cdot n}$, wherein N.sub.n is the number of nucleotides in the first polynucleotide that are substituted, deleted or inserted when compared to the reference polynucleotide, which is X.sub.n nucleotides in length.

7. A process for producing a MurD polypeptide comprising the step of culturing the host cell of claim 6 under conditions suitable for production of said MurD polypeptide, wherein the first polynucleotide encodes a reference polypeptide comprising (a) the amino acid sequence of SEQ ID NO:2, or (b) an amino acid sequence identical to the amino acid sequence of SEQ ID NO:2 except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO:2, the reference polypeptide has a substitution, deletion or insertion of one amino acid.

8. A method for producing antibodies in a mammal which comprises the steps of:

(a) delivering to a tissue of the mammal a nucleic acid vector that expresses in vivo the MurD polypeptide from the isolated polynucleotide of claim 1, or fragment thereof, wherein the polypeptide or polypeptide fragment is effective to induce an immunological response to a polypeptide of SEQ ID NO:2; and

(b) expressing said MurD polypeptide, or a fragment thereof in vivo and inducing an immunological response to produce antibody thereto.

13. A process for producing a MurD polypeptide comprising the step of culturing the host cell of claim 12 under conditions suitable for production of said polypeptide.

14. An isolated polynucleotide comprising a first polynucleotide or the complement of the entire length of said first polynucleotide, wherein said first polynucleotide has at least 99% identity relative to a reference polynucleotide encoding the same mature polypeptide as expressed by the MurD gene contained in the *Streptococcus pneumoniae* 0100993 contained in NCLMB Deposit No. 40794, wherein % identity is calculated as $\frac{\text{times.100}}{N.\text{sub}.n}$, wherein $N.\text{sub}.n$ is the number of nucleotides in the first polynucleotide that are substituted, deleted or inserted when compared to the reference polynucleotide, which is $X.\text{sub}.n$ nucleotides in length.

15. The isolated polynucleotide of claim 14, wherein the first polynucleotide encodes the same mature polypeptide as expressed by the MurD gene contained in *Streptococcus pneumoniae* 0100993 contained in NCLMB Deposit No. 40794, or the full complement of entire length of said first polynucleotide sequence.

18. A process for producing a MurD polypeptide comprising the step of culturing the host cell of claim 17 under conditions suitable for production of said polypeptide, wherein the first polynucleotide encodes a reference polypeptide comprising (a) the amino acid sequence of SEQ ID NO:2, or (b) an amino acid sequence identical to the amino acid sequence of SEQ ID NO:2 except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO:2, the reference polypeptide has a substitution, deletion or insertion of one amino acid.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequence	Abstract	Claims	KWIC	Draw D
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☐ 5. Document ID: US 5891621 A

L1: Entry 5 of 6

File: USPT

Apr 6, 1999

DOCUMENT-IDENTIFIER: US 5891621 A

TITLE: Metabolic pathway assay

CLAIMS:

10. The kit according to claim 9 wherein the first enzyme is the gene product of murC, the second enzyme is the gene product of murD, the third enzyme is the gene product of murE, and the fourth enzyme is the gene product of murF.

15. The kit according to claim 14 wherein the first enzyme is the gene product of murA, the second enzyme is the gene product of murB, the third enzyme is the gene product of murC, the fourth enzyme is the gene product of murD, the fifth enzyme is the gene product of MurE, and the sixth enzyme is the product of MurF.

29. The method according to claim 28 wherein the first enzyme is the gene product of murC, the second enzyme is the gene product of murD, the third enzyme is the gene product of murE, and the fourth enzyme is the gene product of murF.

35. The method according to claim 34 wherein the first enzyme is the gene product

of murA, the second enzyme is the gene product of murB, the third enzyme is the gene product of murC, the fourth enzyme is the gene product of murD, the fifth enzyme is the gene product of murE, and the sixth enzyme is the product of murF.

37. A high-throughput in vitro screening method for detecting a biologically active compound which is comprised of:

(a) combining an enzyme cascade comprising a first enzyme, a second enzyme, a third enzyme, a fourth enzyme, a fifth enzyme and a sixth enzyme, and a labeled substrate for the first enzyme with a compound suspected of having biological activity; wherein:

the first enzyme is the gene product of murA, the second enzyme is the gene product of murB, the third enzyme is the gene product of murC, the fourth enzyme is the gene product of murD, the fifth enzyme is the gene product of murE, and the sixth enzyme is the product of murF; and

(b) measuring the concentrations of the products of the enzymes and comparing to a standard, by absorbing the product of the sixth enzyme onto resin and detecting the amount of label and comparing the amount of label to control.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Attachment	Claims	RMK	Draw. De
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☐ 6. Document ID: US 5681694 A

L1: Entry 6 of 6

File: USPT

Oct 28, 1997

DOCUMENT-IDENTIFIER: US 5681694 A

TITLE: Murd protein method and kit for identification of inhibitors

CLAIMS:

1. A substantially pure MurD protein from *Streptococcus pneumoniae* having the amino acid sequence: ##STR2## which is SEQ ID NO 2.

2. A method for identifying inhibitory compounds of *Streptococcus pneumoniae* MurD protein activity, comprising the steps of:

a) admixing in a suitable reaction buffer

i) a substantially pure MurD protein as claimed in claim 1;

ii) a suitable substrate;

iii) a test inhibitory compound;

b) measuring by any suitable means the amount of product formed; and

c) comparing the amount of product formed with a control in which no test inhibitory compound is present.

5. A kit useful for identifying inhibitors of stem peptide biosynthesis said kit comprising in separate containers:

a) a substantially pure MurD protein, as claimed in claim 1; and

b) a suitable substrate for said protein.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. De
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Terms	Documents
mur.d.clm.	6

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☐ 1. Document ID: US 6211161 B1

L6: Entry 1 of 2

File: USPT

Apr 3, 2001

DOCUMENT-IDENTIFIER: US 6211161 B1

TITLE: UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase (MURD) of staphylococcus aureus

Brief Summary Text (2):

This invention relates to newly identified polynucleotides and polypeptides, and their production and uses, as well as their variants, agonists and antagonists, and their uses. In particular, the invention relates to polynucleotides and polypeptides of the UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase family, as well as their variants, hereinafter referred to as "murD," "murD polynucleotide (s)," and "murD polypeptide(s)" as the case may be.

Brief Summary Text (7):

UDP-N-acetylmuramoylalanine-D-glutamate ligase (D-glutamate adding enzyme) is one of the enzymes involved in the biosynthesis of peptidoglycan. It catalyses the addition of D-glutamate to UDP-N-acetylmuramoyl-L-alanine. This is coupled to the cleavage of ATP into ADP and inorganic phosphate (El-Sherbeini, M., Geissler, W. M., Pittman, J., Yuan, X., Wong, K. K., and Pompliano, D. L. (1998) Cloning and expression of *Staphylococcus aureus* and *Streptococcus pyogenes* murD genes encoding uridine diphosphate N-acetylmuramoyl-L-alanine:D-glutamate ligases, Gene 210:117-125; Mengin-Lecreulx, D. and van Heijenoort, J. (1990) Nucleotide sequence of the murD gene encoding the UDP-MurNAc-L-Ala-D-Glu synthetase of *Escherichia coli*. Nucleic Acids Research 18:183). Discovery of a *Staphylococcus aureus* gene encoding a UDP-N-acetylmuramoylalanine-D-glutamate ligase-like protein which is expressed in vivo implies that there is a role for this protein during infection.

Brief Summary Text (20):

MurD polypeptide of the invention is substantially phylogenetically related to other proteins of the UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase family.

Other Reference Publication (1):

El-Sherbeini, et al., "Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine: D-glutamate ligase (murD) gene, complete cds", GenBank Submission, Accession No. AF009671, Jul. 23, 1997.

Other Reference Publication (3):

El-Sherbeini, et al., "Cloning and expression of *Staphylococcus aureus* and *Streptococcus pyogenes* murD genes uridine diphosphate N-acetylmuramoyl-L-alanina:D-glutamate ligases", Gene, vol. 210, pp. 117-125, (1998).

Other Reference Publication (6):

Pucci, et al., Identification of bacterial UDP-N-acetyl muramyl-L-alanine: D-glutamate ligases. Abstracts of the 97.sup.th General Meeting of the American Society for Microbiology, May, 04-08, 1997, p. 360, abstract K-108.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequence	Attachments	Claims	KWIC	Draw. De
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☐ 2. Document ID: US 6030996 A

L6: Entry 2 of 2

File: USPT

Feb 29, 2000

DOCUMENT-IDENTIFIER: US 6030996 A

TITLE: Mur D inhibiting compounds, compositions containing such compounds and methods of use

Brief Summary Text (2):

UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase (Mur D) is an enzyme which is involved in bacterial peptidoglycan biosynthesis. This enzyme is part of the Mur enzyme pathway.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequence	Attachments	Claims	KWIC	Draw. De
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UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase

2

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L6: Entry 1 of 2

File: USPT

Apr 3, 2001

US-PAT-NO: 6211161

DOCUMENT-IDENTIFIER: US 6211161 B1

TITLE: UDP-N-acetylmuramoyl-l-alanine:D-glutamate ligase (MURD) of staphylococcus aureus

DATE-ISSUED: April 3, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Beattie; David T	Boston	MA		
Deresiewicz; Robert L	Boston	MA		
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Palmer; Leslie Marie	Audubon	PA		
Pratt; Julie M	Wigston			GB
Lonetto; Michael A	Collegeville	PA		
Hodgson; John E	Paris			FR

ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE CODE
Brigham & Women's Hospital	Boston	MA			02
Virus Research Institute	Cambridge	MA			02
SmithKline Beecham Corporation	Philadelphia	PA			02
SmithKline Beecham plc,				GB	03

APPL-NO: 09/ 147928 [PALM]

DATE FILED: March 19, 1999

PARENT-CASE:

RELATED APPLICATIONS This application claims benefit of U.S. Provisional Patent Application No. 60/061,064 filed Oct. 3, 1997.

PCT-DATA:

APPL-NO	DATE-FILED	PUB-NO	PUB-DATE	371-DATE	102 (E) -DATE
PCT/US98/20773	October 2, 1998	WO99/17794	Apr 15, 1999	Mar 19, 1999	Mar 19, 1999

INT-CL: [07] A61 K 48/00, C07 H 21/00, C12 N 15/31, C12 N 15/52, C12 N 15/63

US-CL-ISSUED: 514/44; 435/69.1, 435/252.3, 435/254.11, 435/325, 435/320.1, 435/455, 435/471, 536/23.1, 536/23.2, 536/23.4, 536/23.7

US-CL-CURRENT: 514/44; 435/252.3, 435/254.11, 435/320.1, 435/325, 435/455, 435/471, 435/69.1, 536/23.1, 536/23.2, 536/23.4, 536/23.7

FIELD-OF-SEARCH: 435/69.1, 435/320.1, 435/252.3, 435/254.11, 435/325, 435/455, 435/471, 536/23.1, 536/23.2, 536/23.4, 536/23.7, 514/44

PRIOR-ART-DISCLOSED:

OTHER PUBLICATIONS

El-Sherbeini, et al., "Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine: D-glutamate ligase (murD) gene, complete cds", GenBank Submission, Accession No. AF009671, Jul. 23, 1997.

Mengin-Lecreulx, et al., "Nucleotide sequence of the murD gene encoding the UDP-MurNAc-L-Ala-D-Glu synthetase of Escherichia coli", Nucleic Acids Research, vol. 18, No. 1, p. 183, Oxford University Press 1990.

El-Sherbeini, et al., "Cloning and expression of Staphylococcus aureus and Streptococcus pyogenes murD genes uridine diphosphate N-acetylmuramoyl-L-alanine:D-glutamate ligases", Gene, vol. 210, pp. 117-125, (1998).

Pucci, et al., "Staphylococcus aureus strain ATCC 8325-4 cell wall/cell division gene cluster, yllB, yllC, yllD, pbpA, murD, div1B, ftsA and ftsZ genes, complete cds.", GenBank Submission, Accession No. U94706, Jun. 3, 1997.

Pucci, et al., "Identification and Characterization of Cell Wall-Cell Division Gene Clusters in Pathogenic Gram-Positive Cocci", Journal of Bacteriology, vol. 179, No. 17, pp. 5632-5635, Sep. 1997.

Pucci, et al., Identification of bacterial UDP-N-acetyl muramyl-L-alanine: D-glutamate ligases. Abstracts of the 97th General Meeting of the American Society for Microbiology, May, 04-08, 1997, p. 360, abstract K-108.

ART-UNIT: 162

PRIMARY-EXAMINER: Priebe; Scott D.

ATTY-AGENT-FIRM: Gimmi; Edward R. Deibert; Thomas S. King; William T.

ABSTRACT:

The invention provides murD polypeptides and polynucleotides encoding murD polypeptides and methods for producing such polypeptides by recombinant techniques. Also provided are methods for utilizing murD polypeptides to screen for antibacterial compounds.

17 Claims, 0 Drawing figures

First Hit

L7: Entry 1 of 4

File: PGPB

May 8, 2003

PGPUB-DOCUMENT-NUMBER: 20030088061
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030088061 A1

TITLE: Materials and methods to modulate ligand binding/enzymatic activity of
alpha/beta proteins containing an allosteric regulatory site

PUBLICATION-DATE: May 8, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Staunton, Donald E.	Kirkland	WA	US	

APPL-NO: 09/ 976935 [PALM]
DATE FILED: October 12, 2001

RELATED-US-APPL-DATA:

Application is a non-provisional-of-provisional application 60/239750, filed
October 12, 2000,

INT-CL: [07] A61 K 31/165, C07 K 14/435

US-CL-PUBLISHED: 530/350; 514/617
US-CL-CURRENT: 530/350

REPRESENTATIVE-FIGURES: NONE

ABSTRACT:

Methods of modulating binding between an .alpha./.beta. protein and a binding
partner are provided, along with methods of identifying modulators and their use.

CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of U.S. Provisional Application Serial
No. 60/239,750, filed Oct. 12, 2000.

Day : Monday
Date: 3/29/2004
Time: 11:58:03

 **PALM INTRANET**

Biotech Query for 09/701229

Title: MURD PROTEIN AND GENE OF PSEUDOMONAS AERUGINOSA

Inventor: EL-SHERBEINI, MOHAMMED

Location:

Location Date: Group Art Unit: 1645

Status: 71/RESPONSE TO NON-FINAL OFFICE ACTION ENTERED AND
FORWARDED TO EXAMINER

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[\[Sequence\]](#)
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Entry information

Entry name **MURD_PSEAE**
 Primary accession number **Q9HVZ9**
 Secondary accession number **Q9EY46**
 Entered in Swiss-Prot in **Release 42, October 2003**
 Sequence was last modified in **Release 42, October 2003**
 Annotations were last modified in **Release 42, October 2003**

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD or PA4414**
 From **Pseudomonas aeruginosa [TaxID: 287]**
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.**

References

- [1] SEQUENCE FROM NUCLEIC ACID, AND CHARACTERIZATION.
 MEDLINE=21178826; PubMed=11281713; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Azzolina B.A.](#), [Yuan X.](#), [Anderson M.S.](#), [El-Sherbeini M.](#);
 "The cell wall and cell division gene cluster in the Mra operon of *Pseudomonas aeruginosa*: cloning, production, and purification of active enzymes."
[Protein Expr. Purif.](#) 21:393-400(2001).
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=ATCC 15692 / PAO1;
 MEDLINE=20437337; PubMed=10984043; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Stover C.K.](#), [Pham X.-Q.T.](#), [Erwin A.L.](#), [Mizoguchi S.D.](#), [Warrener P.](#), [Hickey M.J.](#), [Brinkman F.S.L.](#), [Hufnagle W.O.](#), [Kowalik D.J.](#), [Lagrou M.](#), [Garber R.L.](#), [Goltry L.](#), [Tolentino E.](#), [Westbrock-](#)

- Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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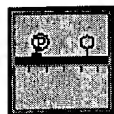
Cross-references

EMBL	AY008276 ; AAG45237.1 ; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE004856 ; AAG07802.1 ; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	G83094 ; G83094 .
HSSP	P14900 ; 1E0D . [HSSP ENTRY / PDB]
CMR	Q9HVZ9 ; PA4414 .
HAMAP	MF_00639 ; -. 1. PBIL [Family / Alignment / Tree] IPR005762 ; MurD.
InterPro	IPR000713 ; Mur_ligase. IPR004101 ; Mur_ligase_C. Graphical view of domain structure .
Pfam	PF01225 ; Mur_ligase; 1. PF02875 ; Mur_ligase_C; 1. Pfam graphical view of domain structure .
TIGRFAMs	TIGR01087 ; murD; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q9HVZ9 .
ProtoNet	Q9HVZ9 .
ProtoMap	Q9HVZ9 .
PRESAGE	Q9HVZ9 .
DIP	Q9HVZ9 .
ModBase	Q9HVZ9 .
SMR	Q9HVZ9 ; 0CFF8F1A7676B266 .
SWISS-2DPAGE	Get region on 2D PAGE .
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	116	122	7	ATP (Potential).
CONFLICT	57	57		V -> A (in Ref. 1).
CONFLICT	260	260		D -> G (in Ref. 1).

Sequence information

Length: 448 Molecular weight: 48080 CRC64: 0CFF8F1A7676B266 [This is a checksum on the sequence]

AA	Da				
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MSLIASDHFR	IVVGLGKSGM	SLVRYLARRG	LPFAVVDTRE	NPPELATLRA	QYPQVEVRCG
70	80	90	100	110	120
ELDAEFLCSA	RELYVSPGLS	L RTPALVQAA	AKGVRISGDI	DLFAREAKAP	IVAITGSNAK
130	140	150	160	170	180
STVTTLVGEM	AVAADKRVAV	GGNLGTPALD	LLADDIELYV	LELSSFQLET	CDRLNAEVAT
190	200	210	220	230	240
VLNVSEDHMD	RYDGMADYHL	AKHRIFRGAR	QVVVNRADAL	TRPLIADTVP	CWSFGLNKP
250	260	270	280	290	300
FKAFLIEED	GQKWLAQFD	KLLPVGELKI	RGAHNYSNAL	AALALGHAVG	LPFDAMLGAL
310	320	330	340	350	360
KAFSGLAHRC	QWVRERQGV	YYDDSKATNV	GAALAAIEGL	GADIDGKLV	LAGGDGKGAD
370	380	390	400	410	420
FHDLREPVAR	FCRAVLLGR	DAGLIAQALG	NAVPLVRVAT	LDEAVRQAAE	LAREGDAVLL
430	440				
SPACASLDMF	KNFEERGRLF	AKAVEELA			

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Entry information

Entry name **MURD_ENTHR**
 Primary accession number **O07669**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 36, July 1998
 Sequence was last modified in Release 36, July 1998
 Annotations were last modified in Release 42, October 2003

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD**
 From Enterococcus hirae [TaxID: 1354]
 Taxonomy Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=S185;
 MEDLINE=99449055; PubMed=10520745; [NCBI, ExPASy, EBI, Israel, Japan]
Duez C., Thamm I., Sapunaric F., Coyette J., Ghuyssen J.-M.;
 "The division and cell wall gene cluster of *Enterococcus hirae* S185.";
 DNA Seq. 9:149-161(1998).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.

- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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Cross-references

EMBL	Y13922; CAA74234.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P14900; 1EEH. [HSSP ENTRY / PDB]
HAMAP	MF_00639; -. 1. PBIL [Family / Alignment / Tree]
InterPro	IPR005762; MurD. IPR000713; Mur_ligase. IPR004101; Mur_ligase_C. Graphical view of domain structure.
Pfam	PF01225; Mur_ligase; 1. PF02875; Mur_ligase_C; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01087; murD; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	O07669 .
ProtoNet	O07669 .
ProtoMap	O07669 .
PRESAGE	O07669 .
DIP	O07669 .
ModBase	O07669 .
SMR	O07669 ; C054CE9046A754AD.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding.

Features



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Key	From	To	Length	Description
NP_BIND	123	129	7	ATP (<i>Potential</i>).

Sequence information

Length: **460** Molecular weight: **50282** CRC64: **C054CE9046A754AD** [This is a checksum on the AA Da sequence]

10	20	30	40	50	60
MTGNEKNFNH	SKTKKVLVLG	LAKSGFSAAK	LLHEL GALVT	VNDGKPFDEK	PEAQELLSLG

```

      70          80          90          100          110          120
      *|          |          |          |          |          |
VKVIAGSHPI ELLDEEFSLM VKNPGIPYSH PFVQKAQELG IPVITEVELA YEVAECPIIG

      130          140          150          160          170          180
      |          |          |          |          |          |
ITGTNGKTTT TTMTGLLLNA GDLPGTARLA GNIGYPASSV AQEATADDKI VMELSSFQLM

      190          200          210          220          230          240
      |          |          |          |          |          |
GITDFRPHVA VVTNIYEAHI DYHKTRKEYV KAKWHLQQNM TEKDYILILNW NQEELRELSK

      250          260          270          280          290          300
      |          |          |          |          |          |
KTKATVLPFA TEQKLPGKAC SLDGSIYYNQ EKIMDITELG VPGSHNVENA LAAISVAKLY

      310          320          330          340          350          360
      |          |          |          |          |          |
GISNEAIKNA LHHFHGVPFR TQYVGEFQGR KFYNSKATN ILATKMALSG FQLDQLVLIA

      370          380          390          400          410          420
      |          |          |          |          |          |
GGLDRGNSFD ELIPALKGIC ALITFGETQN RLEDAGKKAG IPVIKTAENA EAAVPIALEL

      430          440          450          460
      |          |          |          |
SEEGDSILLS PANASWDQYP NFEIRGERFM EAVNKLTIQK

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Entry information

Entry name **MURD_PSEPK**
 Primary accession number **Q88N78**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 43, March 2004
 Sequence was last modified in Release 43, March 2004
 Annotations were last modified in Release 43, March 2004

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD or PP1335**
 From ***Pseudomonas putida* (strain KT2440) [TaxID: 160488]**
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=22423060; PubMed=12534463; [NCBI, ExPASy, EBI, Israel, Japan]
 Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.;
 "Complete genome sequence and comparative analysis of the metabolically versatile *Pseudomonas putida* KT2440.";
 Environ. Microbiol. 4:799-808(2002).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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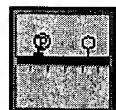
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Cross-references

EMBL	AE016779; AAN66958.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
TIGR	PP1335; -.
HAMAP	MF_00639; -. 1. PBIL [Family / Alignment / Tree]
InterPro	IPR000713 ; Mur_ligase. IPR004101 ; Mur_ligase_C. Graphical view of domain structure.
Pfam	PF01225 ; Mur_ligase; 1. PF02875 ; Mur_ligase_C; 1. Pfam graphical view of domain structure.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q88N78 .
ProtoNet	Q88N78 .
ProtoMap	Q88N78 .
PRESAGE	Q88N78 .
DIP	Q88N78 .
ModBase	Q88N78 .
SMR	Q88N78 ; 1B49F06C2913E915.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features

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Key	From	To	Length	Description
NP_BIND	118	124	7	ATP (<i>Potential</i>).

Sequence information

Length: **450** Molecular weight: **48300** CRC64: **1B49F06C2913E915** [This is a checksum on the
AA Da sequence]

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      |           |           |           |           |           |
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      70           80           90          100          110          120
      |           |           |           |           |           |
CGELDVDFLC RANELYVSPG LALATPALQQ AAARGVKLSG DIELFARHAK APIVAISGSN

     130          140          150          160          170          180
      |           |           |           |           |           |
AKSTVTTLVG EMAAKAGKRV AVGGNLGTPA LDLLADDIEL YVLELSSFQL ETTDQLNAEV

     190          200          210          220          230          240
      |           |           |           |           |           |
ATVLNISEDH MDRYSGLPAY HLAKHRIFRG ARQVVVNRQD ALSRPLPVEG RPCWTFGLNP

     250          260          270          280          290          300
      |           |           |           |           |           |
PDFKAFGLRE VDGEKYLAFE FQTLMPAREL KVRGAHNQSN ALAALALGHA AGLPFEPMLE

     310          320          330          340          350          360
      |           |           |           |           |           |
ALREFGGLAH RCQVVRERNG VNWYDDSKAT NVGAALAAIE GLGADIEGKL VLIAGGDGKG

     370          380          390          400          410          420
      |           |           |           |           |           |
AEFTALREPV KRFCRAVVLL GRDAERLAEA LGDAVPLVRV KTLDDAVQQC AELAQAGDAV

     430          440          450
      |           |           |
LLSPACASLD MFKNFEERGR LFAQAAGGLA

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Entry information

Entry name	MURD_CAUCR
Primary accession number	Q9A597
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 42, October 2003
Sequence was last modified in	Release 42, October 2003
Annotations were last modified in	Release 42, October 2003
Name and origin of the protein	
Protein name	UDP-N-acetylmuramoylalanine--D-glutamate ligase
Synonyms	EC 6.3.2.9 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase D-glutamic acid adding enzyme
Gene name	MURD or CC2556
From	<u>Caulobacter crescentus</u> [TaxID: 155892]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Alphaproteobacteria</u> ; <u>Caulobacterales</u> ; <u>Caulobacteraceae</u> ; <u>Caulobacter</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=ATCC 19089 / CB15;

MEDLINE=21173698; PubMed=11259647; [NCBI, ExPASy, EBI, Israel, Japan]

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke
N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J.,
Craven M.B., Khoury H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J.,
Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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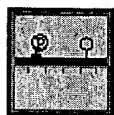
Cross-references

EMBL	AE005924; AAK24527.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	C87566; C87566.
HSSP	P14900; 1E0D. [HSSP ENTRY / PDB]
TIGR	CC2556; -.
HAMAP	MF_00639; -; 1. PBIL [Family / Alignment / Tree] IPR005762 ; MurD. IPR000713 ; Mur_ligase.
InterPro	IPR004101 ; Mur_ligase_C. IPR000205 ; NAD_BS. Graphical view of domain structure.
Pfam	PF01225 ; Mur_ligase; 1. PF02875 ; Mur_ligase_C; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01087 ; murD; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q9A597 .
ProtoNet	Q9A597 .
ProtoMap	Q9A597 .
PRESAGE	Q9A597 .
DIP	Q9A597 .
ModBase	Q9A597 .
SMR	Q9A597 ; DF8215B5EB26D9F9.
SWISS-2DPAGE	Get region on 2D PAGE .
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features



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Key	From	To	Length	Description
NP_BIND	123	129	7	ATP (<i>Potential</i>).

Sequence information

Length: **471** Molecular weight: **49299** CRC64: **DF8215B5EB26D9F9** [This is a checksum on the AA Da sequence]

10	20	30	40	50	60
MIPVRGFEDK	TVAVFGLGRT	GLTAARALIA	GGAKVALWDE	KPASREAAAA	EGFAVVDLQA
70	80	90	100	110	120
ADWSQFAALM	LSPGVPLSHP	KPHWTVEKAR	AAGVEVLGDV	ELFARTVNAA	PAHKRPKIIA
130	140	150	160	170	180
ITGTNGKSTT	TALIGHLCAS	AGRDTRVGGN	IGLGVLGLED	MHGGAVYVLE	LSSYQLDLTS
190	200	210	220	230	240
SLKPDVAVLL	NISPDHLDRH	GGMDGYIAAK	RRIFLNQKGK	DTAIIGVDDA	WCQQICTEIT
250	260	270	280	290	300
AANRRTIWPI	SAGKAMGRGV	YALQGVLYDA	TGERVVEVAD	ILRARSLPGR	HNWQNAAAAY
310	320	330	340	350	360
AAARAIGISM	QDAVDGLMTF	PGLAHRMETV	GKIGKVRFPV	DSKATNADAA	RQAMSSYPKF
370	380	390	400	410	420
YWIAGGVAKA	GGIDDLKDLF	PRIAKAYLIG	EAAEPFSWTL	AGKAECVLSG	TLEKAVQQAY
430	440	450	460	470	
ADAAASGEEA	IVLLSPACAS	FDQFSDFEAR	GEAFRAAVNG	LTAGGGKAAV	A

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Entry information

Entry name **Q82AD8**
 Primary accession number **Q82AD8**
 Secondary accession numbers None
 Entered in TrEMBL in Release 24, June 2003
 Sequence was last modified in Release 24, June 2003
 Annotations were last modified in Release 26, March 2004

Name and origin of the protein

Protein name **Putative UDP-N-acetylmuramoylalanine-D-glutamate ligase**
 Synonyms None
 Gene name **MURD** or **SAV6120**
 From Streptomyces avermitilis [TaxID: 33903]
 Taxonomy Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948; [NCBI, ExPASy, EBI, Israel, Japan]
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 "Genome sequence of an industrial microorganism *Streptomyces avermitilis*: deducing the ability of producing secondary metabolites."
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).

[2]

SEQUENCE FROM NUCLEIC ACID.

STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562; [NCBI, ExPASy, EBI, Israel, Japan]
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
 "Complete genome sequence and comparative analysis of the industrial microorganism *Streptomyces avermitilis*."

Nat. Biotechnol. 21:526-531(2003).

Comments

None

Cross-references

EMBL [AP005045](#); [BAC73831.1](#); [-.\[EMBL / GenBank / DDBJ\]](#) [[CoDingSequence](#)]
[GO:0005737](#); Cellular component: cytoplasm (*inferred from electronic annotation*).
[GO:0005524](#); Molecular function: ATP binding (*inferred from electronic annotation*).
[GO:0016874](#); Molecular function: ligase activity (*inferred from electronic annotation*).
[GO:0004326](#); Molecular function: tetrahydrofolylpolyglutamate synthase activity (*inferred from electronic annotation*).
GO [GO:0008764](#); Molecular function: UDP-N-acetylmuramoylalanine-D-glutamate ligase activity (*inferred from electronic annotation*).
[GO:0009058](#); Biological process: biosynthesis (*inferred from electronic annotation*).
[GO:0009273](#); Biological process: cell wall biosynthesis (sensu Bacteria) (*inferred from electronic annotation*).
[GO:0009396](#); Biological process: folic acid and derivative biosynthesis (*inferred from electronic annotation*).
CMR [Q82AD8](#); [SAV6120](#).
[IPR001645](#); Fpolygl_synthse.
[IPR005762](#); MurD.
InterPro [IPR000713](#); Mur_ligase.
[IPR004101](#); Mur_ligase_C.
[Graphical view of domain structure](#).
Pfam [PF01225](#); Mur_ligase; 1.
[PF02875](#); Mur_ligase_C; 1.
[Pfam graphical view of domain structure](#).
TIGRFAMs [TIGR01087](#); murD; 1.
PROSITE [PS01011](#); FOLYLPOLYGLU_SYNT_1; UNKNOWN_1.
ProDom [\[Domain structure / List of seq. sharing at least 1 domain\]](#)
HOBACGEN [\[Family / Alignment / Tree\]](#)
ProtoMap [Q82AD8](#).
PRESAGE [Q82AD8](#).
ModBase [Q82AD8](#).
SMR [Q82AD8](#); [8CE63F4FCD3E5913](#).
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UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Ligase; Complete proteome.

Features

None

Sequence information

Length: **467** Molecular weight: **48546** CRC64: **8CE63F4FCD3E5913** [This is a checksum on the
AA Da sequence]

10	20	30	40	50	60

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..MTNWQGKNVT VAGLGVSGIP AARVLHGLGA VVTVVNDGDD ERSRAQAADL EALGITVRLG
      70      80      90      100      110      120
      |      |      |      |      |      |
DGATLPEGTE LIVTPGWQP DKPLFAAAAE AGVPVWGDVE LAWRLRGPGS APWLAVTGTN
      130      140      150      160      170      180
      |      |      |      |      |      |
GKTTTVQMLA SILTAAGLRT AAVGNIGVSL LDAVLGEETY DVLAVELSSY QLHWAPSLRA
      190      200      210      220      230      240
      |      |      |      |      |      |
HSATVLNIAP DHLDWHGSME AYTADKGRIY EGNRVACVYN VADKATEDLV RAADVEEGCR
      250      260      270      280      290      300
      |      |      |      |      |      |
AVGFTLGTGP PSQLGVVEGI LVDRAFVEDR QKNAQELAEV ADVHPPAPHN IANALAAAAL
      310      320      330      340      350      360
      |      |      |      |      |      |
ARAFGVPA SA VRDGLRAFRP DAHRIAHVAD VDGVTYIDDS KATNTHAAEA SLAAYGSIVW
      370      380      390      400      410      420
      |      |      |      |      |      |
IAGGLAKGAS FDELVAKSAQ RLRGVVLIGA DRALIREALA RHAPEVPVVD LDRTDTGAMP
      430      440      450      460
      |      |      |      |
AAVQEARRLA VAGDTVLLAP ACASMDMFAN YNKRGDFAE AVRGLGA

```

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Entry information

Entry name **Q7VQI9**

Primary accession number **Q7VQI9**

Secondary accession numbers None

Entered in TrEMBL in Release 25, October 2003

Sequence was last modified in Release 25, October 2003

Annotations were last modified in Release 26, March 2004

Name and origin of the protein

Protein name **UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase**

Synonym **EC 6.3.2.9**

Gene name **MURD** or **BFL140**

From Candidatus Blochmannia floridanus [TaxID: 203907]

Taxonomy Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.

References

[1] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=22784745; PubMed=12886019; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Gil R.](#), [Silva F.J.](#), [Zientz E.](#), [Delmotte F.](#), [Gonzalez-Candelas F.](#), [Latorre A.](#), [Rausell C.](#), [Kamerbeek J.](#), [Gadau J.](#), [Hoelldobler B.](#), [van Ham R.C.H.J.](#), [Gross R.](#), [Moya A.](#);

"The genome sequence of Blochmannia floridanus: comparative analysis of reduced genomes."; Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).

Comments

None

Cross-references

EMBL [BX248584](#); [CAD83661.1](#); - [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]

[GO:0005737](#); Cellular component: cytoplasm (*inferred from electronic annotation*).

[GO:0016874](#); Molecular function: ligase activity (*inferred from electronic annotation*).

GO [GO:0008764](#); Molecular function: UDP-N-acetylmuramoylalanine-D-glutamate ligase activity (*inferred from electronic annotation*).

GO:0009273; Biological process: cell wall biosynthesis (sensu Bacteria) (*inferred from electronic annotation*).

CMR [Q7VQI9](#); BFL140.
 InterPro [IPR005762](#); MurD.
[Graphical view of domain structure](#).
 TIGRFAMs [TIGR01087](#); murD; 1.
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 ProtoMap [Q7VQI9](#).
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 ModBase [Q7VQI9](#).
 SMR [Q7VQI9](#); D09A989BA266E566.
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 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Ligase; Complete proteome.

Features

None

Sequence information


Length: **444** Molecular weight: **49867** CRC64: **D09A989BA266E566** [This is a checksum on the

AA	Da					sequence]
10	20	30	40	50	60	
MIRKYQKSNV	VIIGFGKTGL	SCLNFFLIRG	VIPKIIDTRQ	YPSEMKNLPS	FVEYCFGRLN	
70	80	90	100	110	120	
DFWILNANLI	VVSPGVRDLH	PIIIIEAMKLG	IEVVGDIELF	VREISAPIIA	ITGSNGKSTV	
130	140	150	160	170	180	
TQLVSKMAKQ	AGWSVGVAGN	IGVPVLSLLK	KQYELYVLEI	SSFQLDVTYS	LRATAATILN	
190	200	210	220	230	240	
ISVDHMDRYP	KGLEEYICSK	KRIYHNSYFC	VVNDSDPLTK	PLLNDGIYHV	SFSMNSKSAD	
250	260	270	280	290	300	
YRLEYKGN	WIVANGEYVL	SCAELKINNC	MNYMNLALS	ALSDIVKIPR	IVSLQVLRFF	
310	320	330	340	350	360	
SGLSHRFQLV	YKNRNVWIN	DSKATNVGAT	KEAINNTIIT	LRDGNLHLLL	GGDGKLANFF	
370	380	390	400	410	420	
ELSCLIKHYA	IHLVCFGKDG	VCLTQSGFND	VFLSNNIIDA	MYIISRRVQR	KDIVLLSPAC	
430	440					

ASLDQFSSFR ARGNLFTYLA QRLG

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Entry information

Entry name **MURD_BACHD**
 Primary accession number **Q9K9S8**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 42, October 2003
 Sequence was last modified in Release 42, October 2003
 Annotations were last modified in Release 42, October 2003

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD or BH2567**
 From **Bacillus halodurans [TaxID: 86665]**
 Taxonomy **Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=C-125 / JCM 9153;

MEDLINE=20512582; PubMed=11058132; [NCBI, ExpASY, EBI, Israel, Japan]

Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;

"Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.";

Nucleic Acids Res. 28:4317-4331(2000).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP +

- phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
 - **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
 - **SIMILARITY:** Belongs to the murCDEF family.

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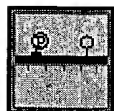
Cross-references

EMBL	AP001515; BAB06286.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	G83970; G83970.
HSSP	P14900; 1UAG. [HSSP ENTRY / PDB]
CMR	Q9K9S8; BH2567.
HAMAP	MF_00639; -; 1. PBIL [Family / Alignment / Tree] IPR005762; MurD.
InterPro	IPR000713; Mur_ligase. IPR004101; Mur_ligase_C. Graphical view of domain structure.
Pfam	PF01225; Mur_ligase; 1. PF02875; Mur_ligase_C; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01087; murD; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q9K9S8.
ProtoNet	Q9K9S8.
ProtoMap	Q9K9S8.
PRESAGE	Q9K9S8.
DIP	Q9K9S8.
ModBase	Q9K9S8.
SMR	Q9K9S8; 76D54C6F549FB2ED.
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Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features



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Key	From	To	Length	Description
NP_BIND	118	124	7	ATP (Potential).

Sequence information

Length: 450 Molecular weight: 48756 CRC64: 76D54C6F549FB2ED [This is a checksum on the AA Da sequence]

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MKHTEQFHQK HILVLGLAKS GEAAARLLHD LGAIIVTVNDQ KPLADNPQAQ KLQKEGIHVV

      70           80           90          100          110          120
      |           |           |           |           |           |
CGEHPISLLD GKELVVKNPQ IRYDNPIVEE AIKRGISVVT EVELASKVSE AEIVAITGSN

      130          140          150          160          170          180
      |           |           |           |           |           |
GKTTTTSLVV EMLKGSAREP KVAGNIGVVA SDVAREATAD DVIVMEVSSF QLMGTSHFRP

      190          200          210          220          230          240
      |           |           |           |           |           |
KVAILLNIFD AHLDYHGSKE NYVAAKKKIV ENMKEEDYFV YNADDPLVSK VAAETKATPI

      250          260          270          280          290          300
      |           |           |           |           |           |
PFSRSTVVKV GAYVDGETYM FRGEKIVEKG DVVLPGDHNV DNVLAAMSAA LLMGATKEQI

      310          320          330          340          350          360
      |           |           |           |           |           |
HHVLSTFSGV EHRLQFVGTA FERKQWYNSK ATNILSTTAA IQSFTDPIVL LAGGLDRGNS

      370          380          390          400          410          420
      |           |           |           |           |           |
FDDLIPALQK VKAVVLFGET KHKLAQAAME AGVETIVEAE RVEDAVRKAL DVSANGDVIL

      430          440          450
      |           |           |
LSPACASWDQ YRTFEERGEA FVTSIEGLQE

```

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Entry information

Entry name	MURD_RICCN
Primary accession number	Q92I60
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 42, October 2003
Sequence was last modified in	Release 42, October 2003
Annotations were last modified in	Release 43, March 2004
Name and origin of the protein	
Protein name	UDP-N-acetylmuramoylalanine--D-glutamate ligase
Synonyms	EC 6.3.2.9 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase D-glutamic acid adding enzyme
Gene name	MURD or RC0560
From	<i>Rickettsia conorii</i> [TaxID: 781]
Taxonomy	Bacteria ; Proteobacteria ; Alphaproteobacteria ; Rickettsiales ; Rickettsiaceae ; Rickettsieae ; Rickettsia .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Malish 7;
MEDLINE=21442074; **PubMed**=11557893; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Ogata H.](#), [Audic S.](#), [Renesto-Audiffren P.](#), [Fournier P.-E.](#), [Barbe V.](#), [Samson D.](#), [Roux V.](#), [Cossart P.](#), [Weissenbach J.](#), [Claverie J.-M.](#), [Raoult D.](#);
 "Mechanisms of evolution in *Rickettsia conorii* and *R. prowazekii*."; [Science](#) 293:2093-2098(2001).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP +

- phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
 - **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
 - **SIMILARITY:** Belongs to the murCDEF family.

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Cross-references

EMBL	AE008617; AAL03098.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	H97769 ; H97769 .
CMR	Q92I60 ; RC0560 .
HAMAP	MF_00639 ; atypical; 1. PBIL [Family / Alignment / Tree] IPR005762 ; MurD.
InterPro	IPR000713 ; Mur_ligase. IPR004101 ; Mur_ligase_C. Graphical view of domain structure.
Pfam	PF01225 ; Mur_ligase; 1. PF02875 ; Mur_ligase_C; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01087 ; murD; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q92I60 .
ProtoNet	Q92I60 .
ProtoMap	Q92I60 .
PRESAGE	Q92I60 .
DIP	Q92I60 .
ModBase	Q92I60 .
SMR	Q92I60 ; 024B268F6074822C .
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features



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Key	From	To	Length	Description
NP_BIND	111	117	7	ATP (<i>Potential</i>).
DOMAIN	260	306	47	RPE3 insert.

Sequence information

Length: **500** Molecular weight: **55787** CRC64: **024B268F6074822C** [This is a checksum on the
AA Da sequence]

```

      10           20           30           40           50           60
      |           |           |           |           |           |
MNSHTKQKIG VFGLGKTGIS VYEELQNKYD VIVYDDLKAN RDIFEELYSK TAIAALSDSR

      70           80           90          100          110          120
      |           |           |           |           |           |
WQNLDITIVLS PGIPLTHEIV NIAKSFNIPI TSDIDLLFAK SKNLKFIAIT GTNGKSTTTA

     130          140          150          160          170          180
      |           |           |           |           |           |
LISHILNSSG LDYPVAGNIG VSALQAKASK DGYVLELSSF QLDLVKTFTA KIAVLLNITP

     190          200          210          220          230          240
      |           |           |           |           |           |
DHLDRHQDMT CYIAAKSKIF DRMDQESYAV INIDNDYCRE VFIKLQEQOR IKLIPFSVAQ

     250          260          270          280          290          300
      |           |           |           |           |           |
ILENGISVVD DKISANFCDD ISFELQHNSE SFRQDEFQGE PAEPECIKIR EHRQDLQNSL

     310          320          330          340          350          360
      |           |           |           |           |           |
VSSFMHYAVP FNKNLQGVHN CENIAASYAV AKIIGVEPKK ILESISSFQS LPHRMQYIGS

     370          380          390          400          410          420
      |           |           |           |           |           |
INNISFYNDS KATNAISAVQ SIKALDNIYW LAGGIPKEGG IEEIKPYFSH IKKAYFYGQA

     430          440          450          460          470          480
      |           |           |           |           |           |
KEIFANTAKN IVDFVICDNL EQAFDLAYKD AVGDNAEIKN ILLAPSCSSY DQFKNFEERG

     490          500
      |           |
ELFIKLC SILRGLITGSS

```

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RESULT 9

US-09-557-884-1

; Sequence 1, Application US/09557884

; Patent No. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

Alignment Scores:

Cr. ID:	0.212	Length:	1830121
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.12%	Indels:	0
DB:	4	Gaps:	0

US-09-701-229-2 (1-448) x US-09-557-884-1 (1-1830121)

Oy 157 GluLeuTyrValLeuGluLeuSerSerPheGlnLeuGluThr 170

Db 1203588 GAACCTTATGTACTAGAGCTTTCTAGTTTTCAGCTTGAGACA 1203629

RESULT 10


US-09-643-990A-1

; Sequence 1, Application US/09643990A

; Patent No. 6528289

; GENERAL INFORMATION:

~~the~~
polypeptide
with identity
to SEQID1
fragment
and comprises
> 25 NA of
SEQID1
+ encodes an
amino
acid
sequence
of SEQID2.

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Entry information

Entry name **MURD_ECOLI**
 Primary accession number **P14900**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 14, April 1990
 Sequence was last modified in Release 20, November 1991
 Annotations were last modified in Release 43, March 2004

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD or B0088**
 From **Escherichia coli [TaxID: 562]**
 Taxonomy **[Bacteria](#); [Proteobacteria](#); [Gammaproteobacteria](#); [Enterobacteriales](#); [Enterobacteriaceae](#); [Escherichia](#).**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=K12;

MEDLINE=90192099; PubMed=2179861; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Ikeda M.](#), [Wachi M.](#), [Ishino F.](#), [Matsushashi M.](#);

"Nucleotide sequence involving murD and an open reading frame ORF-Y spacing murF and ftsW in Escherichia coli.";

[Nucleic Acids Res.](#) 18:1058-1058(1990).

[2]

SEQUENCE FROM NUCLEIC ACID.

STRAIN=K12;

MEDLINE=90174916; PubMed=2129548; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Mengin-Lecreulx D.](#), [van Heijenoort J.](#);

"Nucleotide sequence of the murD gene encoding the UDP-MurNAc-L-Ala-D-Glu synthetase of *Escherichia coli*.";

Nucleic Acids Res. 18:183-183(1990).

[3] SEQUENCE FROM NUCLEIC ACID.

Flouret B.;

Submitted (MAR-1990) to the EMBL/GenBank/DDBJ databases.

[4] SEQUENCE FROM NUCLEIC ACID.

STRAIN=K12;

MEDLINE=92334977; PubMed=1630901; [NCBI, ExPASy, EBI, Israel, Japan]

Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.;

"Systematic sequencing of the *Escherichia coli* genome: analysis of the 0-2.4 min region.";

Nucleic Acids Res. 20:3305-3308(1992).

[5] SEQUENCE FROM NUCLEIC ACID.

STRAIN=K12 / MG1655;

MEDLINE=97426617; PubMed=9278503; [NCBI, ExPASy, EBI, Israel, Japan]

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

"The complete genome sequence of *Escherichia coli* K-12.";

Science 277:1453-1474(1997).

[6] SEQUENCE OF 375-437 FROM NUCLEIC ACID.

STRAIN=K12;

MEDLINE=90036736; PubMed=2509435; [NCBI, ExPASy, EBI, Israel, Japan]

Ikeda M., Sato T., Wachi M., Jung H.K., Ishino F., Kobayashi Y., Matsuhashi M.;

"Structural similarity among *Escherichia coli* FtsW and RodA proteins and *Bacillus subtilis* SpoVE protein, which function in cell division, cell elongation, and spore formation, respectively.";

J. Bacteriol. 171:6375-6378(1989).

[7] SEQUENCE OF 1-19.

STRAIN=K12;

MEDLINE=92111492; PubMed=1765076; [NCBI, ExPASy, EBI, Israel, Japan]

Pratviel-Sosa F., Mengin-Lecreulx D., van Heijenoort J.;

"Over-production, purification and properties of the uridine diphosphate N-acetylmuramoyl-L-alanine:D-glutamate ligase from *Escherichia coli*.";

Eur. J. Biochem. 202:1169-1176(1991).

[8] X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).

MEDLINE=97361823; PubMed=9218784; [NCBI, ExPASy, EBI, Israel, Japan]

Bertrand J.A., Auger G., Fanchon E., Martin L., Blanot D., van Heijenoort J., Dideberg O.;

"Crystal structure of UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase from *Escherichia coli*.";

EMBO J. 16:3416-3425(1997).

[9] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=20425115; PubMed=10966819; [NCBI, ExPASy, EBI, Israel, Japan]

Bertrand J.A., Fanchon E., Martin L., Chantalat L., Auger G., Blanot D., van Heijenoort J., Dideberg O.;

"'Open' structures of MurD: domain movements and structural similarities with folylpolyglutamate synthetase.";

J. Mol. Biol. 301:1257-1266(2000).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA).

- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic.
- **SIMILARITY:** Belongs to the murCDEF family.

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Cross-references

EMBL	X51584; CAA35933.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X17609; CAA35611.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X55034; CAA38865.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	M30807; AAA83858.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	D10483; BAB96656.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE000118; AAC73199.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	S08396; CEECME.
PDB	1E0D; 09-JUN-00. [ExPASy / RCSB / EBI]
	1EEH; 17-JAN-01. [ExPASy / RCSB / EBI]
	1UAG; 18-MAR-98. [ExPASy / RCSB / EBI]
	2UAG; 25-FEB-00. [ExPASy / RCSB / EBI]
	3UAG; 28-JUN-00. [ExPASy / RCSB / EBI]
	4UAG; 15-MAR-00. [ExPASy / RCSB / EBI]
	Detailed list of linked structures.
EcoGene	EG10620 ; murD.
EcoCyc	EG10620 ; murD.
CMR	P14900 ; B0088.
HAMAP	MF_00639 ; -. 1.
	PBIL [Family / Alignment / Tree]
InterPro	IPR005762 ; MurD.
	IPR000713 ; Mur_ligase.
	IPR004101 ; Mur_ligase_C.
	Graphical view of domain structure.
Pfam	PF01225 ; Mur_ligase; 1.
	PF02875 ; Mur_ligase_C; 1.
	Pfam graphical view of domain structure.
TIGRFAMs	TIGR01087 ; murD; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P14900 .
ProtoNet	P14900 .
ProtoMap	P14900 .
PRESAGE	P14900 .
DIP	P14900 .
ModBase	P14900 .
SMR	P14900 ; 18660F69D27717DA.
SWISS-2DPAGE	Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; 3D-structure; Complete proteome.

Features



[Feature table viewer](#)

Key	From	To	Length	Description
INIT_MET	0	0		
NP_BIND	<u>111</u>	<u>117</u>	7	ATP (<i>Potential</i>).
CONFLICT	<u>27</u>	<u>27</u>		R -> A (in Ref. <u>2</u>).
CONFLICT	<u>173</u>	<u>173</u>		A -> T (in Ref. <u>2</u>).
CONFLICT	<u>275</u>	<u>276</u>		AL -> RV (in Ref. <u>2</u>).
TURN	<u>4</u>	<u>5</u>	2	
STRAND	<u>8</u>	<u>11</u>	4	
HELIX	<u>15</u>	<u>25</u>	11	
TURN	<u>26</u>	<u>28</u>	3	
STRAND	<u>32</u>	<u>35</u>	4	
TURN	<u>41</u>	<u>42</u>	2	
HELIX	<u>43</u>	<u>45</u>	3	
TURN	<u>48</u>	<u>49</u>	2	
STRAND	<u>52</u>	<u>54</u>	3	
STRAND	<u>56</u>	<u>56</u>	1	
HELIX	<u>59</u>	<u>63</u>	5	
TURN	<u>64</u>	<u>64</u>	1	
STRAND	<u>67</u>	<u>70</u>	4	
TURN	<u>72</u>	<u>73</u>	2	
TURN	<u>76</u>	<u>77</u>	2	
HELIX	<u>79</u>	<u>86</u>	8	
TURN	<u>87</u>	<u>88</u>	2	
STRAND	<u>90</u>	<u>92</u>	3	
HELIX	<u>94</u>	<u>101</u>	8	
STRAND	<u>106</u>	<u>110</u>	5	
HELIX	<u>115</u>	<u>128</u>	14	
TURN	<u>129</u>	<u>130</u>	2	
STRAND	<u>133</u>	<u>137</u>	5	
TURN	<u>138</u>	<u>140</u>	3	
STRAND	<u>141</u>	<u>141</u>	1	
HELIX	<u>143</u>	<u>146</u>	4	
TURN	<u>149</u>	<u>150</u>	2	
STRAND	<u>153</u>	<u>157</u>	5	
HELIX	<u>160</u>	<u>164</u>	5	
TURN	<u>165</u>	<u>165</u>	1	
STRAND	<u>173</u>	<u>176</u>	4	
HELIX	<u>184</u>	<u>186</u>	3	
TURN	<u>188</u>	<u>189</u>	2	

HELIX	<u>190</u>	<u>199</u>	10
HELIX	<u>200</u>	<u>202</u>	3
TURN	<u>203</u>	<u>204</u>	2
STRAND	<u>207</u>	<u>211</u>	5
TURN	<u>212</u>	<u>213</u>	2
HELIX	<u>215</u>	<u>217</u>	3
STRAND	<u>227</u>	<u>230</u>	4
STRAND	<u>237</u>	<u>240</u>	4
STRAND	<u>247</u>	<u>250</u>	4
TURN	<u>251</u>	<u>252</u>	2
STRAND	<u>253</u>	<u>257</u>	5
HELIX	<u>258</u>	<u>260</u>	3
HELIX	<u>266</u>	<u>281</u>	16
TURN	<u>282</u>	<u>283</u>	2
HELIX	<u>286</u>	<u>295</u>	10
TURN	<u>300</u>	<u>301</u>	2
STRAND	<u>304</u>	<u>309</u>	6
TURN	<u>310</u>	<u>311</u>	2
STRAND	<u>312</u>	<u>316</u>	5
TURN	<u>318</u>	<u>319</u>	2
HELIX	<u>323</u>	<u>330</u>	8
TURN	<u>331</u>	<u>332</u>	2
STRAND	<u>339</u>	<u>344</u>	6
STRAND	<u>346</u>	<u>346</u>	1
TURN	<u>348</u>	<u>349</u>	2
HELIX	<u>353</u>	<u>358</u>	6
STRAND	<u>364</u>	<u>369</u>	6
TURN	<u>371</u>	<u>372</u>	2
HELIX	<u>373</u>	<u>377</u>	5
TURN	<u>378</u>	<u>379</u>	2
HELIX	<u>381</u>	<u>383</u>	3
STRAND	<u>384</u>	<u>386</u>	3
HELIX	<u>390</u>	<u>397</u>	8
HELIX	<u>398</u>	<u>400</u>	3
TURN	<u>403</u>	<u>404</u>	2
STRAND	<u>406</u>	<u>409</u>	4
STRAND	<u>414</u>	<u>414</u>	1
TURN	<u>416</u>	<u>418</u>	3
HELIX	<u>424</u>	<u>437</u>	14

Sequence information

Length: **437** Molecular weight: **46842** CRC64: **18660F69D27717DA** [This is a checksum on the sequence]
AA **Da**

10	20	30	40	50	60
ADYQGKNVVI	IGLGLTGLSC	VDFFLARGVT	PRVMDTRMTP	PGLDKLPEAV	ERHTGSLNDE
70	80	90	100	110	120
WLMAADLIVA	SPGIALAHPS	LSAAADAGIE	IVGDIELFCR	EAQAPIVAIT	GSNGKSTVTT

```

      130      140      150      160      170      180
      |       |       |       |       |       |
LVGEMAKAAG VNVGVGGNIG LPALMLLDDE CELYVLELSS FQLETTSSLQ AVAATILNVT

      190      200      210      220      230      240
      |       |       |       |       |       |
EDHMDRYPFG LQQYRAAKLR IYENAKVCVV NADDALTMPI RGADERCVSF GVNMGDYHLN

      250      260      270      280      290      300
      |       |       |       |       |       |
HQQGETWLRV KGEKVLNVKE MKLSGQHNYT NALAALALAD AAGLPRASSL KALTTFTGLP

      310      320      330      340      350      360
      |       |       |       |       |       |
HRFEVVLEHN GVRWINDSKA TNVGSTEAL NGLHVDGTLH LLLGGDGKSA DFSPLARYLN

      370      380      390      400      410      420
      |       |       |       |       |       |
GDNVRLYCFG RDGAQLAALR PEVAEQTETM EQAMRL LAPR VQPGDMVLLS PACASLDQFK

      430
      |
NFEQRGNEFA RLAKELG

```

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Entry information

Entry name **MURD_HAEIN**
 Primary accession number **P45063**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 32, November 1995
 Sequence was last modified in Release 32, November 1995
 Annotations were last modified in Release 42, October 2003

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD** or **HI1136**
 From **Haemophilus influenzae** [TaxID: 727]
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; **PubMed**=7542800; [NCBI, ExPASy, EBI, Israel, Japan]

[Fleischmann R.D.](#), [Adams M.D.](#), [White O.](#), [Clayton R.A.](#), [Kirkness E.F.](#), [Kerlavage A.R.](#), [Bult C.J.](#),
[Tomb J.-F.](#), [Dougherty B.A.](#), [Merrick J.M.](#), [McKenney K.](#), [Sutton G.](#), [Fitzhugh W.](#), [Fields C.A.](#),
[Gocayne J.D.](#), [Scott J.D.](#), [Shirley R.](#), [Liu L.-I.](#), [Glodek A.](#), [Kelley J.M.](#), [Weidman J.F.](#), [Phillips C.A.](#),
[Spriggs T.](#), [Hedblom E.](#), [Cotton M.D.](#), [Utterback T.R.](#), [Hanna M.C.](#), [Nguyen D.T.](#), [Saudek D.M.](#),
[Brandon R.C.](#), [Fine L.D.](#), [Fritchman J.L.](#), [Fuhrmann J.L.](#), [Geoghagen N.S.M.](#), [Gnehm C.L.](#),
[McDonald L.A.](#), [Small K.V.](#), [Fraser C.M.](#), [Smith H.O.](#), [Venter J.C.](#);

"Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd."; *Science* 269:496-512(1995).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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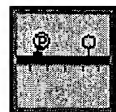
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Cross-references

EMBL	U32793; AAC22791.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	B64185; B64185.
HSSP	P14900; 1E0D. [HSSP ENTRY / PDB]
TIGR	HI1136; -.
HAMAP	MF_00639; -. 1. PBIL [Family / Alignment / Tree] IPR005762 ; MurD. IPR000713 ; Mur_ligase. IPR004101 ; Mur_ligase_C. Graphical view of domain structure.
InterPro	PF01225 ; Mur_ligase; 1. PF02875 ; Mur_ligase_C; 1. Pfam graphical view of domain structure.
Pfam	TIGR01087 ; murD; 1.
TIGRFAMs	[Domain structure / List of seq. sharing at least 1 domain]
ProDom	[Family / Alignment / Tree]
HOBACGEN	P45063.
BLOCKS	P45063.
ProtoNet	P45063.
ProtoMap	P45063.
PRESAGE	P45063.
DIP	P45063.
ModBase	P45063.
SMR	P45063; B7232D573856880B.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features

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Key	From	To	Length	Description
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NP_BIND 112 118 7 ATP (Potential).

Sequence informationLength: **437** Molecular weight: **47906** CRC64: **B7232D573856880B** [This is a checksum on the AA Da sequence]

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MNAYQKNIT I IGLGKTGLS CVDYLLSQQA NIRVIDTRKN PTGIDKLPQN IPLHTGSLNQ

      70      80      90     100     110     120
      |      |      |      |      |      |
EWLLES DMIV ISPGLAVKTP EIQTALKAGV EVIGDIEFC RAATKPIVGI TGSNGKSTVT

     130     140     150     160     170     180
      |      |      |      |      |      |
TLVYEMAKAA GVKVGMGGNI GIPALSLLNE DCELYVLELS SFQLETTYSL KAAAATVLNV

     190     200     210     220     230     240
      |      |      |      |      |      |
TEDHMDRYMD LEDYRQAKLR IYHNAKVGVL NNEDRLTFGE NENQAKHTVS FAENSADYWL

     250     260     270     280     290     300
      |      |      |      |      |      |
KTENGKQYLM VKDEVILPCE EATLVGRHNY MNILAATALA QAIGINLDSI RTALRHFKGL

     310     320     330     340     350     360
      |      |      |      |      |      |
DHRFQLVHQA NGIRWINDSK ATNVGSTVAA LAGLYIEGKL HLLLGGDGKG ADFSELAELI

     370     380     390     400     410     420
      |      |      |      |      |      |
NQPHIICYCF GRDGALLAKF SSQSYLFDTM EQAIEFLRPT LQSGDMVLLS PACASLDQFA

     430
      |
SFEKRGEEFT HLAQCLT

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Entry information

Entry name **Q9ZHB0**
 Primary accession number **Q9ZHB0**
 Secondary accession numbers None
 Entered in TrEMBL in Release 10, May 1999
 Sequence was last modified in Release 10, May 1999
 Annotations were last modified in Release 25, October 2003

Name and origin of the protein

Protein name **D-glutamic acid adding enzyme MurD**
 Synonyms None
 Gene name **MURD**
 From Streptococcus pneumoniae [TaxID: 1313]
 Taxonomy Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=G54;

MEDLINE=99061199; PubMed=9846742; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Massidda O.](#), [Anderluzzi D.](#), [Friedli L.](#), [Feger G.](#);

"Unconventional organization of the division and cell wall gene cluster of *Streptococcus pneumoniae*.";

Microbiology 144:3069-3078(1998).

Comments

None

Cross-references

EMBL [AF068902](#); [AAC95449.1](#); -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]

HSSP [P14900](#); 1UAG. [[HSSP ENTRY](#) / [PDB](#)]

[GO:0005737](#); Cellular component: cytoplasm (*inferred from electronic annotation*).

[GO:0005524](#); Molecular function: ATP binding (*inferred from electronic annotation*).

GO [GO:0016874](#);Molecular function: ligase activity (*inferred from electronic annotation*).
[GO:0008764](#);Molecular function: UDP-N-acetylmuramoylalanine-D-glutamate ligase activity (*inferred from electronic annotation*).
[GO:0009058](#);Biological process: biosynthesis (*inferred from electronic annotation*).
[GO:0009273](#);Biological process: cell wall biosynthesis (sensu Bacteria) (*inferred from electronic annotation*).

InterPro [IPR005762](#); MurD.
[IPR000713](#); Mur_ligase.
[IPR004101](#); Mur_ligase_C.
[Graphical view of domain structure.](#)

Pfam [PF01225](#); Mur_ligase; 1.
[PF02875](#); Mur_ligase_C; 1.
[Pfam graphical view of domain structure.](#)

TIGRFAMs [TIGR01087](#); murD; 1.

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HOBACGEN [\[Family / Alignment / Tree\]](#)

ProtoMap [Q9ZHB0.](#)

PRESAGE [Q9ZHB0.](#)

ModBase [Q9ZHB0.](#)

SMR [Q9ZHB0](#); 048D2CA5964F06BF.

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UniRef [View cluster of proteins with at least 50% / 90% identity.](#)

Keywords

None

Features

None

Sequence information

Length: **450** Molecular weight: **48490** CRC64: **048D2CA5964F06BF** [This is a checksum on the
 AA Da sequence]

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70	80	90	100	110	120
TGGHPLELLD	EEFALMVKNP	GIPYSNPMIE	KALAKGIPVL	TEVELAYLIS	EAPIIGITGS
130	140	150	160	170	180
NGKTTTTTMI	GEVLTAAGQH	GLLSGNIGYP	ASQVAQIATD	KNTLVMELSS	FQLMGVQEFH
190	200	210	220	230	240
PEIAVITNLM	PTHIDYHGLF	EEYVAAKWNI	QNKMTAADFL	VLNFNQDLVK	DLASKTEATV
250	260	270	280	290	300
VPFSTLEKVD	GAYLEDGQLY	FRGEVMAAN	EIGVPGSHNV	ENALATIAVA	KLRGVDNQTI

```
      310      320      330      340      350      360
      |       |       |       |       |       |
KETLSAFGGV KHRLQFVDDI KGVKFYND SKSTNILATQKA LSGFDNSKVV LIAGGLDRGN

      370      380      390      400      410      420
      |       |       |       |       |       |
EFDELVPDIT GLKKMVILGQ SAERVKRAAD KAGVAYVEAT DIADATRKAY ELATQGDVVL

      430      440      450
      |       |       |
LSPANASWDM YANFEVRGDL FIDTVaelKE
```

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Entry information

Entry name **MURD_ENTFA**

Primary accession number **O07108**

Secondary accession numbers None

Entered in Swiss-Prot in Release 36, July 1998

Sequence was last modified in Release 42, October 2003

Annotations were last modified in Release 42, October 2003

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**

Synonyms **EC 6.3.2.9**

UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme

Gene name **MURD** or **EF0993**

From Enterococcus faecalis (Streptococcus faecalis) [TaxID: 1351]

Taxonomy Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=A24836;

MEDLINE=97431524; PubMed=9287029; [NCBI, ExPASy, EBI, Israel, Japan]

Pucci M.J., Thanassi J.A., Discotto L.F., Kessler R.E., Dougherty T.J.;

"Identification and characterization of cell wall-cell division gene clusters in pathogenic Gram-positive cocci.";

J. Bacteriol. 179:5632-5635(1997).

[2]

SEQUENCE FROM NUCLEIC ACID.

STRAIN=V583 / ATCC 700802;

MEDLINE=22550857; PubMed=12663927; [NCBI, ExPASy, EBI, Israel, Japan]

Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Fouts D.E., Eisen

J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W., Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;

"Role of mobile DNA in the evolution of vancomycin-resistant *Enterococcus faecalis*."; *Science* 299:2071-2074(2003).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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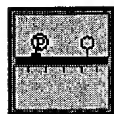
Cross-references

EMBL	U94707; AAC45635.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AE016950; AAO80799.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P14900; 1UAG. [HSSP ENTRY / PDB]
TIGR	EF0993; -.
HAMAP	MF_00639; -; 1. PBIL [Family / Alignment / Tree] IPR005762; MurD.
InterPro	IPR000713; Mur_ligase. IPR004101; Mur_ligase_C. Graphical view of domain structure.
Pfam	PF01225; Mur_ligase; 1. PF02875; Mur_ligase_C; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01087; murD; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	O07108.
ProtoNet	O07108.
ProtoMap	O07108.
PRESAGE	O07108.
DIP	O07108.
ModBase	O07108.
SMR	O07108; DB4E0B9B5514A88D.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	119	125	7	ATP (Potential).
CONFLICT	83	83		P -> L (in Ref. 1).
CONFLICT	165	165		N -> D (in Ref. 1).
CONFLICT	292	292		A -> P (in Ref. 1).
CONFLICT	303	303		R -> K (in Ref. 1).
CONFLICT	305	305		T -> S (in Ref. 1).
CONFLICT	336	336		I -> F (in Ref. 1).
CONFLICT	385	385		E -> K (in Ref. 1).
CONFLICT	394	394		A -> P (in Ref. 1).

Sequence information

Length: 456 Molecular weight: 49698 CRC64: DB4E0B9B5514A88D [This is a checksum on the sequence]

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TGGHPIELLD	EEFELIVKNP	GIPYTNPLVA	EALTRKIPII	TEVELAGQIA	ECPIVGITGT
130	140	150	160	170	180
NGKTTTTTMI	GLLLNADRTA	GEARLAGNIG	FPASTVAQEA	TAKDNLVMEI	SSFQLMGIET
190	200	210	220	230	240
FHPQIAVITN	IFEAHLDYHG	SRKEYVAAKW	AIQKNMTAED	TLILNWNQVE	LQTLAKTTAA
250	260	270	280	290	300
NVLPFSTKEA	VEGAYLLDGK	LYFNEEYIMP	ADELGIPGSH	NIENALAAIC	VAKLKNVSNA
310	320	330	340	350	360
QIRQTLTNFS	GVPHRTQFVG	EVQQRIFYND	SKATNILATE	MALSGFDNOK	LLLLAGGLDR
370	380	390	400	410	420
GNSFDELVPA	LLGLKAIVLF	GETKEKLAEA	AKKANIETIL	FAENVQTAVT	IAFDYSEKDD
430	440	450			
TILLSPACAS	WDQYPNFEVR	GEAFMQAVQQ	LKESEM		

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Entry information

Entry name **MURD_SYNY3**
 Primary accession number **P73668**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 36, July 1998
 Sequence was last modified in Release 36, July 1998
 Annotations were last modified in Release 42, October 2003

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD or SLL2010**
 From **Synechocystis sp. (strain PCC 6803) [TaxID: 1148]**
 Taxonomy **Bacteria; Cyanobacteria; Chroococcales; Synechocystis.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=97061201; PubMed=8905231; [NCBI, ExPASy, EBI, Israel, Japan]
 Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
 DNA Res. 3:109-136(1996).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).

- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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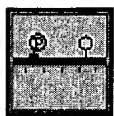
Cross-references

EMBL D90908; BAA17713.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 PIR S77155; S77155.
 HSSP P14900; 1EEH. [[HSSP ENTRY](#) / [PDB](#)]
 CMR P73668; SLL2010.
 HAMAP MF_00639; -, 1.
 PBIL [[Family](#) / [Alignment](#) / [Tree](#)]
 IPR005762; MurD.
 InterPro IPR000713; Mur_ligase.
 IPR004101; Mur_ligase_C.
[Graphical view of domain structure.](#)
 Pfam PF01225; Mur_ligase; 1.
 PF02875; Mur_ligase_C; 1.
[Pfam graphical view of domain structure.](#)
 TIGRFAMs TIGR01087; murD; 1.
 ProDom [[Domain structure](#) / [List of seq. sharing at least 1 domain](#)]
 HOBACGEN [[Family](#) / [Alignment](#) / [Tree](#)]
 BLOCKS P73668.
 ProtoNet P73668.
 ProtoMap P73668.
 PRESAGE P73668.
 DIP P73668.
 ModBase P73668.
 SMR P73668; B31528111A627F10.
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 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features



[Feature table viewer](#)

Key	From	To	Length	Description
NP_BIND	113	119	7	ATP (<i>Potential</i>).

Sequence information

Length: 452 Molecular weight: 49048 CRC64: B31528111A627F10 [This is a checksum on the

AA	Da	sequence]
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MPQACVIGLG	RSGIAAARVL	HRDGWQVTVF
40	50	60
DQADNDQLRH	MGQPLVQEGI	SLKLGDRLLDP
70	80	90
VKEAWPERIV	VSPGVPWDIP	LLVAAREKGV
100	110	120
EVTGELELAW	QYLHAVPWVG	ITGTNGKTTT
130	140	150
TSLVQAIFQK	AGLNAPACGN	IGYAACEVLV
160	170	180
QNQNYDWIVA	EISSYQIESS	PTLAPQIGLW
190	200	210
TTFTPDHLRS	HKTLENYFNI	KASLLSRSAI
220	230	240
QVLNGDDPHL	HSHGPNLYPQ	AHWTSTQGAN
250	260	270
HLAGLCDPKQ	GVYLQDNWVN	AFGELIAPIN
280	290	300
LFKMPGQHNQ	QNLLMAIAAA	RLAGIDKKAI
310	320	330
TETLLTFTGV	PHRLEPICTI	NGVQFINDSK
340	350	360
ATNYDAAEVG	LSSMKGPTIL	IAGGEAKEGD
370	380	390
DQAWLAQIRQ	KAVAVLLIGD	AAPNFATRLK
400	410	420
AVGYENYEIV	ETMANAVQRG	LELASKNNAS
430	440	450
AVLLSPACAS	FDQYNSFEER	GEDFRACCLG
		LV

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or at [NCBI \(USA\)](#)



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[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet \(Java\)](#)




[ScanProsite](#), [MotifScan](#)



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			Taiwan	

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Hosted by NCSC US Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan				
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[\[Features\]](#)
[\[Sequence\]](#)
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Entry information

Entry name **MURD_RHIME**
 Primary accession number **Q52953**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 39, May 2000
 Sequence was last modified in Release 39, May 2000
 Annotations were last modified in Release 42, October 2003

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD** or **R02178** or **SMC01864**
 From **Rhizobium meliloti (Sinorhizobium meliloti) [TaxID: 382]**
 Taxonomy **Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=1021;

MEDLINE=21396507; PubMed=11481430; [NCBI, ExPASy, EBI, Israel, Japan]

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadiou E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Pumelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

[2]

PRELIMINARY SEQUENCE OF 1-344 FROM NUCLEIC ACID.

STRAIN=1021;

MEDLINE=95011665; PubMed=7926844; [NCBI, ExPASy, EBI, Israel, Japan]

Leach F., Wacks D.B., Signer E.R.;

"Rhizobium meliloti homologs of Escherichia coli mur genes.";

Gene 148:87-90(1994).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.
- **CAUTION:** In addition to the conflicts shown below, Ref.2 sequence has 7 frameshift errors scattered along the sequence.

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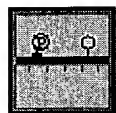
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CMR	Q52953; R02178.	
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	IPR005762; MurD.	
InterPro	IPR000713; Mur_ligase.	
	IPR004101; Mur_ligase_C.	
	Graphical view of domain structure.	
	PF01225; Mur_ligase; 1.	
Pfam	PF02875; Mur_ligase_C; 1.	
	Pfam graphical view of domain structure.	
TIGRFAMs	TIGR01087; murD; 1.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOBACGEN	[Family / Alignment / Tree]	
BLOCKS	Q52953.	
ProtoNet	Q52953.	
ProtoMap	Q52953.	
PRESAGE	Q52953.	
DIP	Q52953.	
ModBase	Q52953.	
SMR	Q52953; E123D25E142D819E.	
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UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	121	127	7	ATP (Potential).
CONFLICT	132	132		I -> V (in Ref. 2).
CONFLICT	243	243		R -> S (in Ref. 2).

Sequence information

Length: **463** Molecular weight: **48066** CRC64: **E123D25E142D819E** [This is a checksum on the sequence]

AA	Da					
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MIPVTSFKGR	KVALFGLGGS	GLATAQALVS	GGADVVAWDD	NPDSVAKAAA	AGIATADLRG	
70	80	90	100	110	120	
ADWHAFAAFV	LSPGVPLTHP	KPHWSVDLAH	QAGVEIIGDV	ELFVRERRKH	APDCPFIAIT	
130	140	150	160	170	180	
GTNGKSTTTA	LIAHILRTSG	RDTQLGGNIG	TAVLTLDPPK	AGRFYVVECS	SYQIDLAPTL	
190	200	210	220	230	240	
DPTAGILLNL	TPDHLDHRGT	MQHYADIKER	LVAGSGTAVV	GVDDSLSSLI	ADRVERAGTK	
250	260	270	280	290	300	
VVRISRRHPL	AEGIYAEGSA	LMRAQDGASS	LFTDLAGIQT	LRGGHNAQNA	AAAIACLAV	
310	320	330	340	350	360	
GISGKDIVDG	LRSFPGPKHR	MQPVAKKGEV	VFVNSKATN	AEAAAPALSS	YDRIYWIAGG	
370	380	390	400	410	420	
LPKEGGITSL	APFFPKIVKA	YLIGEAAPSF	AATLGEAVPY	EISGTLEKAV	AHAAADAARD	
430	440	450	460			
SQGPAVMLS	PACASFDQYK	NFEVRGDAFV	GHVAALEGVS	MLI		

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Entry information

Entry name **MURD_BACSU**
 Primary accession number **Q03522**
 Secondary accession number **Q59246**
 Entered in Swiss-Prot in **Release 27, October 1993**
 Sequence was last modified in **Release 27, October 1993**
 Annotations were last modified in **Release 43, March 2004**

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD or BSU15200**
 From **Bacillus subtilis [TaxID: 1423]**
 Taxonomy **Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=168;
 MEDLINE=93171879; PubMed=8436954; [NCBI, ExPASy, EBI, Israel, Japan]
Daniel R.A., Errington J.;
 "DNA sequence of the murE-murD region of Bacillus subtilis 168.";
 J. Gen. Microbiol. 139:361-370(1993).

[2]

SEQUENCE FROM NUCLEIC ACID.

STRAIN=168;
 MEDLINE=98044033; PubMed=9384377; [NCBI, ExPASy, EBI, Israel, Japan]
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J.,

Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

"The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.";
Nature 390:249-256(1997).

[3] SEQUENCE OF 82-451 FROM NUCLEIC ACID.

STRAIN=168;

MEDLINE=93003529; PubMed=1391053; [NCBI, ExPASy, EBI, Israel, Japan]

Henriques A.O., de Lencastre H., Piggot P.J.;

"A *Bacillus subtilis* morphogene cluster that includes spoVE is homologous to the mra region of *Escherichia coli*.";

Biochimie 74:735-748(1992).

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

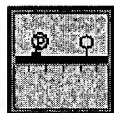
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Cross-references

EMBL	Z15056; CAA78769.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] Z99111; CAB13393.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] X64258; CAA45555.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	D47691; D47691.
HSSP	P14900; 1EEH. [HSSP ENTRY / PDB]
SubtiList	BG10225; murD. [Micado]
CMR	Q03522; BSU15200.
HAMAP	MF_00639; -. 1. PBIL [Family / Alignment / Tree]

InterPro	IPR005762 ; MurD. IPR000713 ; Mur_ligase. IPR004101 ; Mur_ligase_C. Graphical view of domain structure.
Pfam	PF01225 ; Mur_ligase; 1. PF02875 ; Mur_ligase_C; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01087 ; murD; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q03522 .
ProtoNet	Q03522 .
ProtoMap	Q03522 .
PRESAGE	Q03522 .
DIP	Q03522 .
ModBase	Q03522 .
SMR	Q03522 ; 66594D6FF91A3932.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.

Keywords**Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.****Features**

Feature table viewer

Key	From	To	Length	Description
NP_BIND	120	126	7	ATP (<i>Potential</i>).
CONFLICT	342	342		A -> R (in Ref. 3).

Sequence information

Length: **451** Molecular weight: **49650** CRC64: **66594D6FF91A3932** [This is a checksum on the sequence]

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70	80	90	100	110	120
CGEHPVSLFD	QHQITILIKN	PGIPYENIMV	QEAEKRGIPV	WTEIELAYYL	TSAKFIGITG
130	140	150	160	170	180
SNGKTTTTTL	IYEMLKADSQ	KALIAGNIGT	VASEVAYHAD	GDEWIVTELS	SFQLMGTHAF
190	200	210	220	230	240
RPEISLILNV	FDAHLDYHHT	RENYEKAKQK	VYLHQ TASDK	AIVNQDDETV	URLAEAGKAE
250	260	270	280	290	300

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IVPFSVSKTL EQGAYVKDSM IMFNGEAILP LEEVVLPGAH NLENILAAIA VVKTAGASNE
      310      320      330      340      350      360
      |      |      |      |      |      |
AVKKVLTSFT GVKHRLQYVT TVNGRKFYND SKATNILATS KALSAFDKPV ILLAGGLDRG
      370      380      390      400      410      420
      |      |      |      |      |      |
NGFDDLKPYM KHVKAFLTFG QTAPKLEKLG NELGIQHVKR VDNVEQAVSA AFALSNEGDV
      430      440      450
      |      |      |
ILLSPACASW DQFKTFEERG DMFIDAVHML K

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Hosted by NCSC US Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan					
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NiceZyme View of ENZYME: EC 6.3.2.9

Official Name	
UDP-N-acetylmuramoylalanine--D-glutamate ligase.	
Alternative Name(s)	
MurD synthetase. UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase. Uridine diphospho-N-acetylmuramoylalanyl-D-glutamate synthetase. D-glutamate-adding enzyme. D-glutamate ligase. UDP-Mur-NAC-L-Ala:D-Glu ligase.	
Reaction catalysed	
$ \begin{array}{l} \text{ATP} \\ + \text{ UDP-N-acetylmuramoyl-L-alanine} \\ + \text{ glutamate} \\ \hline \text{<=>} \\ \text{ADP} \\ + \text{ phosphate} \\ + \text{ UDP-N-acetylmuramoyl-L-alanyl-D-glutamate} \end{array} $	
Comments	
<ul style="list-style-type: none"> Involved with EC 6.3.2.4, EC 6.3.2.7 or EC 6.3.2.13, EC 6.3.2.8 and EC 6.3.2.10 in the synthesis of a cell-wall peptide. 	
Cross-references	
Biochemical Pathways; map number(s)	O4
BRENDA	6.3.2.9
EMP/PUMA	6.3.2.9
WIT	6.3.2.9
Kyoto University LIGAND chemical database	6.3.2.9
IUBMB Enzyme Nomenclature	6.3.2.9
IntEnz	6.3.2.9
MEDLINE	Find literature relating to 6.3.2.9
	Q8UDM6 , MURD_AGRT5 ; Q8YPS9 , MURD_ANASP ; O67852 , MURD_AQUAE ; Q9K9S8 , MURD_BACHD ; Q03522 , MURD_BACSU ; Q8G4Q6 , MURD_BIFLO ; O51532 , MURD_BORBU ; Q8YI68 , MURD_BRUME ; Q8FZP2 , MURD_BRUSU ; P57313 , MURD_BUCAI ; Q8K9T2 , MURD_BUCAP ; Q89AQ2 , MURD_BUCBP ;

Swiss-Prot

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Q9JSZ5 , MURD_NEIMA;	Q9K0Y4 , MURD_NEIMB;	Q8ER50 , MURD_OCEIH;
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Q52953 , MURD_RHIME;	Q92I60 , MURD_RICCN;	Q9ZDC2 , MURD_RICPR;
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Q9F1N2 , MURD_SHEVI;	O33595 , MURD_STAAM;	Q8NX35 , MURD_STAAW;
Q8CSX6 , MURD_STAEP;	Q8E6P1 , MURD_STRA3;	Q8E186 , MURD_STRA5;
Q9S2W9 , MURD_STRCO;	Q8DVE3 , MURD_STRMU;	Q8P063 , MURD_STRP8;
Q97RU8 , MURD_STRPN;	O68388 , MURD_STRPY;	Q8DQM2 , MURD_STRR6;
Q8DMN8 , MURD_SYNEL;	P73668 , MURD_SYNY3;	Q9WY76 , MURD_THEMA;
Q8R9G4 , MURD_THETN;	O83873 , MURD_TREPA;	Q9KPG5 , MURD_VIBCH;
Q87SG6 , MURD_VIBPA;	Q8DEK8 , MURD_VIBVU;	Q8D2Z4 , MURD_WIGBR;
Q8PII9 , MURD_XANAC;	Q8P775 , MURD_XANCP;	Q9PEB0 , MURD_XYLFA;
Q87EA7 , MURD_XYLFT;	Q8ZIF1 , MURD_YERPE;	

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Entry information

Entry name **MURD_RICPR**
 Primary accession number **Q9ZDC2**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 39, May 2000
 Sequence was last modified in Release 39, May 2000
 Annotations were last modified in Release 42, October 2003

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD** or **RP410**
 From *Rickettsia prowazekii* [TaxID: 782]
 Taxonomy *Bacteria*; *Proteobacteria*; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Rickettsieae*; *Rickettsia*.

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 STRAIN=Madrid E;
 MEDLINE=99039499; PubMed=9823893; [NCBI, ExPASy, EBI, Israel, Japan]
 Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M.,
 Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.;
 "The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria."; *Nature* 396:133-140(1998).

Comments

- FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP +

- phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
- **PATHWAY:** Peptidoglycan biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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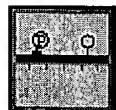
Cross-references

EMBL	AJ235271; CAA14867.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A71699; A71699.
HSSP	P14900; 1UAG. [HSSP ENTRY / PDB]
CMR	Q9ZDC2; RP410.
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InterPro	IPR000713; Mur_ligase. IPR004101; Mur_ligase_C. Graphical view of domain structure.
Pfam	PF01225; Mur_ligase; 1. PF02875; Mur_ligase_C; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01087; murD; 1.
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ProtoNet	Q9ZDC2.
ProtoMap	Q9ZDC2.
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DIP	Q9ZDC2.
ModBase	Q9ZDC2.
SMR	Q9ZDC2; B9CCCF7437FB7AA6.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features



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Key	From	To	Length	Description
NP_BIND	111	117	7	ATP (<i>Potential</i>).

Sequence information

Length: **445** Molecular weight: **50129** CRC64: **B9CCCF7437FB7AA6** [This is a checksum on the
AA Da sequence]

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      |           |           |           |           |           |
MNAYKKQKIG IFGLGKTGIS VYEELKNKYD LIVYDDLEAN RDIFKELFGN NLITVLSDSR

      70           80           90          100          110          120
      |           |           |           |           |           |
WQDLDKIVLS PGVPLTHEVV RIAHHFNIPI ISDIDLFFEK SKNLKFIAIT GTNGKSTTTA

     130          140          150          160          170          180
      |           |           |           |           |           |
LISHILNSNG LDYPVAGNIG VPALQAKASN EGYVLELSSF QLDLVKSFTV KVAVLLNITP

     190          200          210          220          230          240
      |           |           |           |           |           |
DHLDRYQDMN DYIAAKAKIF DRMDKDSYAV INIDNDYCRK IFVLLQKDQS IKLIPFSVTK

     250          260          270          280          290          300
      |           |           |           |           |           |
ILKNGISIVD DKIHNDNLT Y KLPLNKNLQG LHCNENIAAS YAVAKIIGLE SKKILESIS

     310          320          330          340          350          360
      |           |           |           |           |           |
FQSLHHRMQY IGSINNISFY NDSKATNAIS ALQSIKALDN IYWLAGGIPK EGGIEGIPY

     370          380          390          400          410          420
      |           |           |           |           |           |
FNKIKKAYFY GQAKAMFANT AKNIIDFVIC DNLEYAFNIA YKDAVSDTTE VKNILLAPSC

     430          440
      |           |
SSYDQFKNFE ERGELFIKLS KRHWQ

```

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Entry information

Entry name **MURD_STAAM**
 Primary accession number **O33595**
 Secondary accession number **O07323**
 Entered in Swiss-Prot in **Release 36, July 1998**
 Sequence was last modified in **Release 36, July 1998**
 Annotations were last modified in **Release 42, October 2003**

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD or [SAV1183](#) or [SA1026](#)**
 From **[Staphylococcus aureus](#) (strain Mu50 / ATCC 700699)** [TaxID: [158878](#)]
[Staphylococcus aureus](#) (strain N315) [TaxID: [158879](#)]
[Staphylococcus aureus](#) [TaxID: [1280](#)]
 Taxonomy **Bacteria; Firmicutes; Bacillales; Staphylococcus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Mu50 / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146; [NCBI, ExPASy, EBI, Israel, Japan]
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";

Lancet 357:1225-1240(2001).

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=R27;

El-Sherbeini M., Geissler W., Pittman J., Yuan X., Wong K., Pompliano D.;

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

[3] SEQUENCE FROM NUCLEIC ACID.

STRAIN=ATCC 8325-4;

Pucci M.J., Thanassi J.A., Discotto L.F., Kessler R.E., Dougherty T.J.;

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

Comments

- **FUNCTION:** Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA) (*By similarity*).
- **CATALYTIC ACTIVITY:** ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
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- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** Belongs to the murCDEF family.

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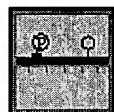
Cross-references

EMBL	AP003361; BAB57345.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
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	AF009671; AAC46291.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	U94706; AAC45626.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	JC6560; JC6560.
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CMR	O33595; SAV1183.
HAMAP	MF_00639; -. 1.
	PBIL [Family / Alignment / Tree]
InterPro	IPR005762; MurD.
	IPR000713; Mur_ligase.
	IPR004101; Mur_ligase_C.
	Graphical view of domain structure .
Pfam	PF01225; Mur_ligase; 1.
	PF02875; Mur_ligase_C; 1.
	Pfam graphical view of domain structure .
TIGRFAMs	TIGR01087; murD; 1.
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BLOCKS	O33595 .
ProtoNet	O33595 .
ProtoMap	O33595 .
PRESAGE	O33595 .
DIP	O33595 .
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SMR [O33595; 071BEEE9CF74F985](#).
 SWISS-2DPAGE [Get region on 2D PAGE](#).
 UniRef [View cluster of proteins with at least 50% / 90% identity](#).

Keywords

Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.

Features

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Key	From	To	Length	Description
NP_BIND	118	124	7	ATP (Potential).
CONFLICT	370	385		RAMVVFQGQTKAKFAKL -> SREWLYSDSRKLSLLNY (in Ref. 3).

Sequence information

Length: **449** Molecular weight: **49843** CRC64: **071BEEE9CF74F985** [This is a checksum on the sequence]

AA	Da					
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MLNYTGLENK	NVLVVGLAKS	GYEAAKLLSK	LGANVTVNDG	KDLSQDAHAK	DLESMGISVV	
70	80	90	100	110	120	
SGSHPLTLLD	NNPIIVKNPG	IPYTVSIIDE	AVKRGLKILT	EVELSYLISE	APIIAVTGTN	
130	140	150	160	170	180	
GKTTVTSLIG	DMFKKSRLTG	RLSGNIGYVA	SKVAQEVKPT	DYLVTELSSF	QLLGIEKYKP	
190	200	210	220	230	240	
HIAIITNIYS	AHLDYHENLE	NYQNAKKQIY	KNQTEEDYLI	CNYHQRQVIE	SEELKAKTLY	
250	260	270	280	290	300	
FSTQQEVDGI	YIKDGFIVYK	GVRIINTEDL	VLPGEHNLEN	ILAAVLACIL	AGVPIKAIID	
310	320	330	340	350	360	
SLTTFSGIEH	RLQYVG TNRT	NKYINDSKAT	NTLATQFALN	SFNQPIIWLC	GGLDRGNEFD	
370	380	390	400	410	420	
ELIPYMENVR	AMVVFQGTKA	KFAKLGNSQG	KSVIEANNVE	DAVDKVQDII	EPNDVVLSP	
430	440					
ACASWDQYST	FEERGEKFIE	RFRAHLPSY				

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Entry information

Entry name **MURD_STAAM**
 Primary accession number **O33595**
 Secondary accession number **O07323**
 Entered in Swiss-Prot in **Release 36, July 1998**
 Sequence was last modified in **Release 36, July 1998**
 Annotations were last modified in **Release 42, October 2003**

Name and origin of the protein

Protein name **UDP-N-acetylmuramoylalanine--D-glutamate ligase**
 Synonyms **EC 6.3.2.9**
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
D-glutamic acid adding enzyme
 Gene name **MURD or SAV1183 or SA1026**
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Staphylococcus aureus (strain N315) [TaxID: 158879]
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MEDLINE=21311952; **PubMed**=11418146; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Kuroda M.](#), [Ohta T.](#), [Uchiyama I.](#), [Baba T.](#), [Yuzawa H.](#), [Kobayashi I.](#), [Cui L.](#), [Oguchi A.](#), [Aoki K.-I.](#),
[Nagai Y.](#), [Lian J.-Q.](#), [Ito T.](#), [Kanamori M.](#), [Matsumaru H.](#), [Maruyama A.](#), [Murakami H.](#), [Hosoyama](#)
[A.](#), [Mizutani-Ui Y.](#), [Takahashi N.K.](#), [Sawano T.](#), [Inoue R.-I.](#), [Kaito C.](#), [Sekimizu K.](#), [Hirakawa H.](#),
[Kuhara S.](#), [Goto S.](#), [Yabuzaki J.](#), [Kanehisa M.](#), [Yamashita A.](#), [Oshima K.](#), [Furuya K.](#), [Yoshino C.](#),
[Shiba T.](#), [Hattori M.](#), [Ogasawara N.](#), [Hayashi H.](#), [Hiramatsu K.](#);
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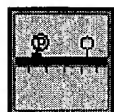
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130	140	150	160	170	180
GKTTVTSLIG	DMFKKSRLTG	RLSGNIGYVA	SKVAQEVKPT	DYLVTELSSF	QLLGIEKYKP
190	200	210	220	230	240
HIAIITNIYS	AHLDYHENLE	NYQNAKKQIY	KNQTEEDYLI	CNYHQRQVIE	SEELKAKTLY
250	260	270	280	290	300
FSTQQEVDGI	YIKDGFIVYK	GVRIINTEDL	VLPGEHNLEN	ILAAVLACIL	AGVPIKAIID
310	320	330	340	350	360
SLTTFSGIEH	RLQYVGTNRT	NKYINDSKAT	NTLATQFALN	SFNQPIIWLC	GGLDRGNEFD
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430	440				
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